

effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
 RT Genome Res. 13: 2265-2270(2003).
 RL Dumoutier L., Louahed J., Renaud J.-C.;
 CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
 in vivo.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
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 CC -!- DR EMBL; AJ277247; CAC06085_1; -.
 CC -!- DR EMBL; AJ277248; CAC19409_1; -.
 CC -!- DR EMBL; AF279437; ARG22064_1; -.
 CC -!- DR EMBL; AF887519; ARK62468_1; -.
 CC -!- DR EMBL; AY08890; AA089249_1; -.
 CC -!- DR GenBank; HGNC:11900; IL22.
 CC -!- DR MIM: 605330; -.
 CC -!- DR GO:0005576; C:extracellular; IC.
 CC -!- DR GO:0045518; F:interleukin-22 receptor binding; NAS.
 CC -!- DR GO:0006953; P:acute-phase response; NAS.
 CC -!- DR GO:0006954; P:cell-cell signaling; IC.
 CC -!- DR InterPro: IPR00098; Interleukin_10.
 CC -!- DR InterPro: PS00520; Interleukin_10_1.
 CC -!- DR Cytokine; Glycoprotein; Signal; Polymorphism.
 CC -!- SIGNAL 1 33 POTENTIAL.
 CC -!- FT CHAIN 34 179 INTERLEUKIN_22.
 CC -!- FT CARBOHYD 54 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -!- FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -!- FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -!- FT VARIANT 158 158 S -> G.
 CC -!- FT SEQUENCE 179 AA; 20011 MW; 3C5E64D60CP8767 CRC64;
 CC -!- SEQUENCE 179 AA; 20011 MW; 3C5E64D60CP8767 CRC64;

Query Match 99.3% Score 897; DB 1; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.7e-78;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAALQKVSSEPLMGLTNSCLLALLVQCGMADISHCRLDKENFQOQYITNRTFLMA 60
 Db 1 MAALQKVSSEPLMGLTNSCLLALLVQCGMADISHCRLDKENFQOQYITNRTFLMA 60
 Qy 61 KEASLADNNTDVRLIGEKLPFGVNSCRLKMQVNFITLEEVLPQSDRQPYMQEYVP 120
 Db 61 KEASLADNNTDVRLIGEKLPFGVNSCRLKMQVNFITLEEVLPQSDRQPYMQEYVP 120
 Qy 121 FIAARSNRLSTCHIS3DLDLHQRYVQKLKDQTVKLGSGEIKAIQGELDLFMSLRNACI 179
 Db 121 FIAARSNRLSTCHIS3DLDLHQRYVQKLKDQTVKLGSGEIKAIQGELDLFMSLRNACI 179
 RESULT 2
 IL22_MOUSE STANDARD; PRT; 179 AA.
 AC Q9JU79; STANDARD; PRT; 179 AA.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Interleukin-22 precursor (IL-TIF) (IL-10-related T-cell-derived
 DE inducible factor) (IL-TIF) (IL-TIF alpha) (Interleukin-22a); (IL-22a).
 GN IL22 OR IL22A OR ILTIFA OR ILTIF.
 OC Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OC [1]_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RP

STRAIN=AKR;
 RX MEDLINE=20126044; PubMed=10657629;
 RA Dumoutier L., Louahed J., Renaud J.-C.;
 RT "Cloning and characterization of IL-10-related T cell-derived
 RT inducible factor (IL-TIF), a novel cytokine structurally related to
 RT IL-10 and inducible by IL-9.";
 RL J. Immunol. 164:1814-1819(2000).
 RN [2]
 RN RP FROM N.A.
 RC STRAIN=L129;
 RX MEDLINE=21069354; PubMed=11197690;
 RA Dumoutier L., Van Roost E., Colau D., Ameye G., Michaux L.,
 RA Renaud J.-C.;
 RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
 RT genes.";
 RL Genes Immun. 1:488-494 (2000).
 CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
 CC -!- in vivo.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
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 CC -!- DR EMBL; AJ249491; CAB75546_1; -.
 CC -!- DR EMBL; AJ24727; CAC19435_1; -.
 CC -!- DR MGI; MGI:1355307; IL22.
 CC -!- DR GO:0005515; P:protein binding; IPI.
 CC -!- DR GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
 CC -!- DR GO:0025116; P:tyrosine phosphorylation of S. . . IDA.
 CC -!- DR InterPro; IPR000098; Interleukin_10.
 CC -!- DR SWARI; SM00188; IL10; 1.
 CC -!- DR FROSTIE; PS00520; INTERLEUKIN_10; 1.
 CC -!- DR FROSTIE; PS00520; INTERLEUKIN 10; 1.
 CC -!- DR Glycoprotein; Signal; Potential.
 CC -!- FT SIGNAL 1 33 POTENTIAL.
 CC -!- FT CHAIN 34 179 INTERLEUKIN_22.
 CC -!- FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -!- FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -!- FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC -!- SQ SEQUENCE 179 AA; 20106 MW; ACB0F557AA79274 CBC64;
 CC -!- Query Match 79.5%; Score 718; DB 1; Length 179;
 CC -!- Best Local Similarity 76.5%; Pred. No. 4.6e-61;
 CC -!- Matches 137; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 MAALQKVSSEPLMGLTNSCLLALLVQCGMADISHCRLDKENFQOQYITNRTFLMA 60
 Db 1 MAVLQKMSSEPLMGLTNSCLLALLVQCGMADISHCRLDKENFQOQYITNRTFLMA 60
 Qy 61 KEASLADNNTDVRLIGEKLPFGVNSCRLKMQVNFITLEEVLPQSDRQPYMQEYVP 120
 Db 61 KEASLADNNTDVRLIGEKLPFGVNSCRLKMQVNFITLEEVLPQSDRQPYMQEYVP 120
 Qy 121 FIAARSNRLSTCHIS3DLDLHQRYVQKLKDQTVKLGSGEIKAIQGELDLFMSLRNACI 179
 Db 121 FIAARSNRLSTCHIS3DLDLHQRYVQKLKDQTVKLGSGEIKAIQGELDLFMSLRNACI 179
 RESULT 3
 IL22_MOUSE STANDARD; PRT; 179 AA.
 AC Q9JU78; STANDARD; PRT; 179 AA.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DB Interleukin-22 precursor (IL-TIF) (IL-10-related T-cell-derived
 DE inducible factor) (IL-TIF) (IL-TIF alpha) (Interleukin-22a); (IL-22a).
 GN IL22B OR ILTIFB.
 OC Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OC [1]_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RP

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBITaxonID=10090;
 RN [1] _SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=0126044; PubMed=10657629;
 RT "Cloning and characterization of IL-10-related T cell-derived
 RT inducible factor (IL-TIF, a novel cytokine structurally related to
 RL "IL-10 and inducible by IL-9".
 RL J. Immunol. 164:1814-1819(2000).
 RN [2] _SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=21069154; PubMed=11197690;
 RA Dumoutier L., Louland J., Renaud J.-C.;
 RA Renaud J.-C.;
 RA Dumoutier L., Van Roost E., Colau D., Ameye G., Michaux L.,
 RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
 RT genes.";
 RL Genes Immun. 1:488-494 (2000).
 CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
 CC -!- in vivo.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
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 DR EMBL; AD49492; CAB30547.1; -.
 DR MGD; MGD:215139; IL10fb.
 DR InterPro; IPR000093; Interleukin_10.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 33 POTENTIAL.
 FT CHAIN 34 179 INTERLEUKIN-22B.
 FT CARCHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARCHYD 58 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARCHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 179 AA; 20162 MW; 442549850DA5F60 CRC64;
 Score 79.1%; Score 71.4; DB 1; Length 179;
 Best Local Similarity 76.0%; Pred. No. 1.1e-0; Gaps 0;
 Matches 136; Conservative 23; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 MAALOKSVSSPLMGTLATCLLALLVQGSAAPISSKDNKNEQQYITINRTFMLA 60
 Db 1 MAVLQKSMSSFLMGTLIAASCCLLIAIAQEAANALPINTRKLEVSNFQQXIVNETFMLA 60
 Qy 61 KEASIAADNTNTDVRIGEKUFGKUFGYSMSRVCYLMQKQVINFTEEVLPQSDRFQYQEVYP 120
 Db 61 KEASIAADNTNTDVRIGEKUFGKUFGYSMSRVCYLMQKQVINFTEEVLPQSDRFQYQEVYP 120
 Qy 121 FLTKLISNLKSLCHIEGDDLHQENYQKLOKOTVKGEGEKAIGLDLFLFMSLIRNAC 179
 Db 121 FLTKLISNLKSLCHIEGDDLHQENYQKLOKOTVKGEGEKAIGLDLFLFMSLIRNAC 179

factor) (CSIF).
 IL10 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=96063015; PubMed=7579578;
 RA Lockhart B., Slobbe L., Droogmans L., Griffin F., Buchan G.;
 RT "The cloning and sequencing of cervine interleukin 10.";
 RL Seg. 5:265-268(1995).
 CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
 CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
 activated macrophages and by helper T cells (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC -!- CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 DR EMBL; U11767; AAA85434.1; -.
 DR HSSP; P22303; LINR.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005141; F:interleukin-10 receptor binding; NAS.
 DR GO; GO:0005916; P:anti-apoptosis; ISS.
 DR GO; GO:0006954; P:inflammatory response; ISS.
 DR InterPro; IPR000098; Interleukin_10.
 DR PRINTS; PRO12726; IL10_1.
 DR PRODom; PD003687; Interleukin_10; 1.
 DR SMART; SM00180; IL10_1.
 DR PROSINS; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 179 INTERLEUKIN-10.
 FT DISULPID 31 127 BY SIMILARITY.
 FT DISULPID 81 133 BY SIMILARITY.
 FT CARBONYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 179 AA; 20467 MW; AIC0035D484B6050 CRC64;
 Score 11.8%; Score 106.5; DB 1; Length 179;
 Best Local Similarity 22.8%; Pred. No. 0.0051; Gaps 6;
 Matches 41; Conservative 32; Mismatches 74; Indels 33; Gaps 6;
 Qy 20 CILLLA-LLVQGAAAPTTSSHCRLLDKSINFOQYITINRTFMLA 68
 Db 10 CLVFLAGVAASRDASADSDDSSC-----THFNSLPLMLRELTAFSRYKNNFFQMKD 60
 Qy 69 NTDVRLJGEKUFGKUFGYSMSRVCYLMQKQVINFTEEVLPQSDRFQYQEVYP 124
 Db 61 QDLSMILTQSLLDFCYGCOALSSEMIOFTLEYVM-POAENHGPEIKEHYNLSLGEKLT 119
 Qy 125 ISNRLSTCHIEGDDLHQENYQKLOKOTVKGEGEKAIGLDLFLFMSLIRNAC 176
 Db 120 LRLRFLRCHREPLPCENKSASKVQVSVFSLQERGTYKANSEFDPIVNTYTYTMKRN 179

RESULT 4
 IL10_CEREL ID IL10_MACFA
 ID IL10 MACFA STANDARD PRT; 178 AA.
 AC P51746; P79318;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DB Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory

RESULT 5
 IL10_MACFA ID IL10_MACFA
 ID IL10 MACFA STANDARD PRT; 178 AA.
 AC P79318;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DB Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory

| | |
|--|----------------|
| DE factor (CSTF). | Qy 174 LRN 176 |
| GN Macaca fasciularis (Crab eating macaque) (Cynomolgus monkey). | Db 176 IRN 178 |
| OS Macaca fasciularis (Crab eating macaque) (Cynomolgus monkey). | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; | |
| OC Cercopithecinae; Macaca. | |
| OX NCBI_TaxID=5541; | |
| DN [1] | |
| RP SEQUENCE FROM N.A. | |
| RA Matsunari, M. | |
| RL Submitted (PEB-1997) to the EMBL/GenBank/DBJ databases. | |
| CC -i- FUNCTION: Initiates the synthesis of a number of cytokines, including IFN-gamma, IL-2, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity). | |
| CC -i- SUBUNIT: Homodimer (By similarity). | |
| CC -i- SUBCELLULAR LOCATION: Secreted. | |
| CC -i- SIMILARITY: Belongs to the IL-10 family. | |
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| CC | |
| DR EBO0054; PAB019132; 1; -. | |
| DR HSSP; P22301; 1; NR. | |
| DR GO; GO:0005576; C: extracellular; ISS. | |
| DR GO; GO:0008189; P: apoptosis inhibitor activity; ISS. | |
| * DR GO; GO:0005141; P: interleukin-10 receptor binding; ISS. | |
| DR GO; GO:0006916; P: anti-apoptosis; ISS. | |
| DR GO; GO:0030183; P: B-cell differentiation; ISS. | |
| DR GO; GO:0042100; P: B-cell proliferation; ISS. | |
| DR GO; GO:0007253; P: cytoplasmic sequestering of NF-kappaB; ISS. | |
| DR GO; GO:0006954; P: inflammatory response; ISS. | |
| DR GO; GO:0045077; P: negative regulation of interferon-gamma bio- . ; ISS. | |
| DR GO; GO:0045467; P: negative regulation of MHC class II biosynt. . ; ISS. | |
| DR GO; GO:0045019; P: negative regulation of nitric oxide biosynt. . ; ISS. | |
| DR GO; GO:0042130; P: negative regulation of T-cell proliferation; ISS. | |
| DR GO; GO:0045191; P: regulation of isotype switching; ISS. | |
| DR GO; GO:0042092; P: T-helper 2 type immune response; ISS. | |
| DR GO; GO:0007280; P: tyrosine phosphorylation of STAT protein; ISS. | |
| DR Interprot: IPB200008; Interleukin_10. | |
| DR P200726; IL10; 1. | |
| DR PR01294; INTRLEUKIN10. | |
| DR PRODOM; ED0001687; Interleukin_10. | |
| DR SMART; SM00138; IL10; 1. | |
| DR PROSITE; PS00520; INTRLEUKIN_10; 1. | |
| KW Cytokine; Glycoprotein; Signal. | |
| PY SIGNAL: 18 POTENTIAL. | |
| PT CHAIN: 19 178 INTERLEUKIN-10. | |
| PT DISULFID: 30 126 BY SIMILARITY. | |
| PT DISULFID: 80 132 BY SIMILARITY. | |
| PT CARBOHYD: 134 2035 MW; N-LINKED (GLCNAC. .) (POTENTIAL). | |
| SEQ SEQUENCE: 178 AA: 3ECD5B3B3BA718 CRC64; | |
| Query Match 11.7% Score 105.5; DB: 1; Length 178; | |
| Best Local Similarity 23.5%; Pred. No. 0.0063; Mismatches 32; Indels 31; Gaps 6; | |
| Matches 43; Conservative | |
| Qy 18 TSCNLLILIVQGGAAP----ISSHCRLDKSN----FQOQYITRTPMLAKEASL 65 | |
| Db 3 SSALICCLCVLILGVTRASPGGTQSENSTCRFPGNLFPMURDLRDAFSRVTKFOMKD-- 59 | |
| Qy 56 ADNNTDWRLJIGKEFQHGVSMSERCYLMKVQINFLTEVLFQPSDRFQPMQEVVYBFLR-- 124 | |
| Db 60 ---QDNLNLLKESLDFKCYLGOALSNTIQFLCEYVM-POAQNHDPIKEHVSQGEN 115 | |
| Qy 125 ---ISMRPLSTCHIEGDDLHTQRTVKIGEGETKAIGELDL-----LMS 173 | |
| Db 116 LKTRLRLRCHRLPCENKSKAVECWNAFSKUQEQGVYKAMSEFDIPIVNEYAMTMK 175 | |
| Qy | |
| Db | |

| Cytokine; Glycoprotein; Signal; 3D-structure. | |
|---|--|
| KW SIGNAL | 1 |
| FT CHAIN | 25 |
| FT DISUFID | 26 |
| FT DISUFID | 170 |
| FT DISUFID | 119 |
| FT CARBHYD | 27 |
| FT CARBHYD | 125 |
| FT TURN | 127 |
| FT TURN | 127 |
| FT HELIX | 127 |
| FT TURN | 30 |
| FT TURN | 31 |
| FT HELIX | 32 |
| FT TURN | 45 |
| FT HELIX | 46 |
| FT HELIX | 48 |
| FT HELIX | 61 |
| FT HELIX | 68 |
| FT TURN | 70 |
| FT TURN | 71 |
| FT HELIX | 72 |
| FT TURN | 85 |
| FT HELIX | 86 |
| FT FT | 86 |
| FT HELIX | 87 |
| FT TURN | 94 |
| FT HELIX | 96 |
| FT HELIX | 98 |
| FT TURN | 99 |
| FT TURN | 118 |
| FT TURN | 120 |
| FT TURN | 122 |
| FT HELIX | 124 |
| FT HELIX | 126 |
| FT HELIX | 130 |
| FT TURN | 141 |
| FT HELIX | 142 |
| FT HELIX | 142 |
| FT TURN | 143 |
| FT TURN | 152 |
| FT TURN | 153 |
| FT HELIX | 153 |
| FT TURN | 154 |
| FT TURN | 166 |
| SEQUENCE | 170 AA; 19914 MW; AE20AE65D358FOCE CRC64; |
| SQ | |
| Query | 11.4%; Score 103; DB 1; Length 170; |
| Best Local Similarity | 24.8%; Pred. No. 0.01; |
| Matches 40; Conservative | 27; Mismatches 68; Indels 26; G |
| QY | 20 CLLLIALLIVQGAAAPISSECRDKNSFQQ-----PYITNRFLMAREASLADN |
| Db | 11 CLVLYLAPCGGG----TIDQG----DNFPOMLRLDRAFSRVCFQD----- |
| QY | 73 RLIGKRLPHGVMSMRCPYCLMKQVLFNFTILEKVLFLPQSDRFQPYMQEVVPIIAR----- |
| Db | 57 LLKESLLEDFKGVLGQALSEMIFYLEVMM-TQAEQNDPEAKDHDVNSLGENLKTT |
| QY | 129 LSTCHIEGDDLHIOQRNQKQKIDTVKIGSEGEIKAIGEIDL 169 |
| Db | 116 LTRRERFTPCKENKSTPKVNAFKLCKGKTYAQSMBPNT 156 |

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DR EMBL; L26630; AA99970.1; -.

DR HSSP; P22301; 1INR.

DR InterPro; IPR00098; Interleukin_10.

DR Pfam; PF00726; IL10; 1.

DR PRNTS; PR01294; INTRLEUKIN10.

DR Problem; PD003687; Interleukin_10; 1.

DR SMART; SM00188; IL10; 1.

DR PROSITE; PS005220; INTRLEUKIN_10; 1.

KW Cytokine; Glycoprotein; Signal.

SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 178 INTERLEUKIN-10.

FT DISULFID 30 126 BY SIMILARITY.

FT DISULFID 80 132 BY SIMILARITY.

FT CARBHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 178 AA; 20585 MW; 35DE86528AB718 CRC64;

Query Match 11.2%; Score 101.5; DB: 1; Length 178;

Best Local Similarity 24.1%; Pred. No. 0.015; Gaps 6;

Matches 41; Conservative 30; Mismatches 72; Indels 27; Gaps 6;

Qy 18 TSCHILLALIVQGAAAP-----ISSHCRDLDSNFOQPYITN-----RTFMLEAKEA 63

Db 3 SSALICLVLITGLTRASPGQGTQENSENCTRFPGNL-PEMIDLRLDVSFRVKTFQMQKD- 59

Qy 64 SLADNNDTDVRLIGEKLPHGYSMSERCYLMQKVINFTEVLYTFQDSDRFQPYMQBVYPIA 123

Db 60 -----QLDNLILKESLILDPKPGYLGQCALESQIYFLVEWM-POARNHBDIKEHVNLSLG 113

Qy 124 R----ISNRLSTCHIEGDDLHLIQRNVQKUDTVKKGESCEIKATIGELDL 169

Db 114 ENLKTLRLRLRCCRFLPCBNKSAVEQVNAFSLQEKGVYKAMSBFDI 163

RESULT 8

IL10_MACMU STANDARD; PRT; 178 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Interleukin-10 precursor (IL10) (Cytokine synthesis inhibitor factor) [CSIF].

DE IL10.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi;

OC Macromia; Rutherfordia; Primates; Catarrhini; Cercopitheciidae;

OC Cercopithecinae; Macaca.

NCBI_TaxID=5544;

[1]

RN SEQUENCE FROM N.A.

RN STRAIN:PTC 2;

RX MB011396003435; PubMed=756110;

RX Willinger, P.J.; Brar, S.S.; Mayne, A.E.; Chikkala, N.; Ansari, A.A.;

RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."

J. Immunol. 155:3946-3954 (1995).

RT -; FUNCTION: Inhibits the synthesis of a number of cytokines, including TNF gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).

RT -; SUBUNIT: Homodimer (By similarity).

RT -; SUBCELLULAR LOCATION: Secreted.

RT -; SIMILARITY: Belongs to the IL10 family.

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CC EMBL: M26029; AAA99975_1; -

DR HSSP; P23301; 2ILK.

DR GO; GO:0007676; C: extracellular; ISS.

DR GO; GO:0008159; F: apoptosis inhibitor activity; ISS.

DR GO; GO:0005141; F: Interleukin-10 receptor binding; ISS.

DR GO; GO:0006916; Plant-apoptosis; ISS.

DR GO; GO:0030133; P: B-cell differentiation; ISS.

DR GO; GO:0042100; P: B-cell proliferation; ISS.

DR GO; GO:0007257; P: cytoplasmic sequencing of NF-kappaB; ISS.

DR GO; GO:0030057; P: hemopoiesis; ISS.

DR GO; GO:0006954; P: inflammatory response; ISS.

DR GO; GO:0045077; P: negative regulation of interferon-gamma bio.

DR GO; GO:0045347; P: negative regulation of MHC class II biogeny; ISS.

DR GO; GO:0045191; P: negative regulation of nitric oxide biogeny; ISS.

DR GO; GO:0042130; P: negative regulation of T-cell proliferation; ISS.

DR GO; GO:0045191; P: regulation of isotype switching; ISS.

DR GO; GO:0042092; P: T-helper 2 type immune response; ISS.

DR InterPro; IPR000098; P: tyrosine phosphorylation of STAT protein; ISS.

DR InterPro; IPR000098; Interleukin_10.

DR Pfam; PF00726; IIL10; 1.

DR PRODOM; PR01294; INTRLEUKIN10.

DR SMART; SM00188; IIL10; 1.

DR PROSITE; PS00520; INTERLEUKIN_10; 1.

DR Cytokine; Glycoprotein; Signal.

DR SIGNAL; 18 POTENTIAL.

DR FT CHAIN; 19 178 INTERLEUKIN-10.

DR DISULFID; 30 126 BY SIMILARITY.

DR DISULFID; 80 132 BY SIMILARITY.

DR CARBOHYD; 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR SEQUENCE; 178 AA; 20557 MW;

DR 35CC0D9BB3BBA713 CRC64;

DR 35CC0D9BB3BBA713 CRC6

"Cloning, sequencing of human interleukin-10 cDNA and construction of its eukaryotic expression vector." Harbin Yike Daxue Xue Bao 35:4-6 (2001).

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| | | |
|--|---|-----------------------------------|
| [4] | SEQUENCE FROM H.A. | DR EMBL; M57627; AAK63207; 1; |
| Rieder M.-J., Carrington J.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A., Submitted (SEP-2001) to the EMBL/GenBank/DDJB databases. | DR EMBL; U16720; AAK80104; 1; - | |
| [5] | SEQUENCE OF 26-34 AND 179-178 | DR EMBL; AY029171; AAK38162; 1; - |
| MEDLINE=9070801; PubMed=240562; | DR EMBL; AF418271; AAL06594; 1; - | |
| Gesser B., Leffers H., Jinquan T., Vestergaard C., Kirstein N., Baldwin S., Paliwal S., Mui P.W., Pramanik B., Trobta P.P.; Sindet-Pedersen S., Jensen S.L., Thestrup-Pedersen K., Larsen C.G.; "Identification of functional domains on human interleukin 10.,"; Proc. Natl. Acad. Sci. U.S.A. 94:14620-14625 (1997).; | DR EMBL; A38580; A38580; DR EMBL; 1ILK; 10-JUL-95; DR EMBL; 2ILK; 14-OCT-96; DR EMBL; 1INR; 14-OCT-96; DR EMBL; 1J7V; 19-SEP-01; DR EMBL; 1ILK3; 17-JUL-02; DR Genew; HGNC:5962; IL10.; | |
| [6] | DISULFIDE BONDS. | DR MIM; 124092; - |
| MEDLINE=9337205; PubMed=8364628; | DR MIM; 266600; - | |
| Windsor W.T., Syto R., Tsarogouios A., Zhang R., Durkin J., Baldwin S., Paliwal S., Mui P.W., Pramanik B., Trobta P.P.; "Disulfide bond assignments and secondary structure analysis of human and murine interleukin 10.,"; Biochemistry 32:8807-8815(1993). | DR GO; GO:0000515; C: extracellular space; TAS. DR GO; GO:0005625; C: soluble fraction; TAS. DR GO; GO:0008189; P: apoptosis inhibitor activity; NAS. DR GO; GO:0005125; P: cytokine activity; TAS. DR GO; GO:0005141; P: interleukin-10 receptor binding; NAS. DR GO; GO:0008916; P: anti-apoptosis; NAS. DR GO; GO:0030183; P: B-cell differentiation; NAS. DR GO; GO:0042100; P: B-cell proliferation; NAS. DR GO; GO:0008935; P: chemotaxis; TAS. DR GO; GO:0007253; P: cytoplasmic sequestering of NF-kappaB; NAS. DR GO; GO:00005197; P: hemopoiesis; TAS. DR GO; GO:0008954; P: inflammatory response; NAS. DR GO; GO:0045155; P: negative regulation of interferon-gamma bio. NAS. DR GO; GO:0045077; P: negative regulation of interferon-gamma bio. NAS. DR GO; GO:0045347; P: negative regulation of nitric oxide biosyn. DR GO; GO:0045019; P: negative regulation of nitric oxide biosyn. DR GO; GO:0042130; P: negative regulation of T-cell proliferation; NAS. DR GO; GO:0008284; P: positive regulation of cell proliferation; TAS. DR GO; GO:0045191; P: regulation of isotype switching; NAS. DR GO; GO:0007165; P: signal transduction; TAS. DR GO; GO:0042092; P: T-helper 2 type immune response; TAS. DR Interpro; IPR000098; Interleukin_10.; | |
| [7] | X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). | DR Pfam; PF00726; IL10; 1. |
| MEDLINE=96032603; PubMed=7547951; | DR PRINTS; PR01294; INTERLEUKIN10. | |
| Walter M.R., Nagabushan T.L., "Crystal structure of interleukin 10 reveals an interferon gamma-like fold.,"; Biochemistry 34:1218-1225(1995). | DR PRODOM; PD00368; Interleukin_10; 1. | |
| [8] | X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS). | DR SMART; SM00188; IL10; 1. |
| MEDLINE=96173008; PubMed=859020; | DR PROSITE; PS00520; INTERLEUKIN10; 1. | |
| Zdanov A., Schalk-Hihi C., Gustchina A., Tsang M., Weatherbee J., Wlodawer A.; "Crystal structure of interleukin-10 reveals the functional dimer with an unexpected topological similarity to interferon gamma.,"; Structure 3:51-60(1995).; | DR Cytokine; Glycoprotein; Signal; Disease mutation; 3D-structure. KW SIGNAL; 1 | |
| [9] | X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS). | FT SIGNAL; 1 |
| MEDLINE=97052966; PubMed=8897595; | FT CHAIN; 19 | |
| Schalk-Hihi C., Wlodawer A.; "Crystal structure of human interleukin-10 at 1.6-A resolution and a model of complex with its soluble receptor.,"; Protein Sci. 5:1955-1962(1996).; | FT DISULFID; 19 | |
| [10] | VARIANT CD ARG-15. | FT DISULFID; 178 |
| MEDLINE=2270949; PubMed=12825869; | FT DISULFID; 30 | |
| van der Linde K., Boor P.P., Sandkuijl L.A., Meijissen M.A., Savelkoul H.F., Wilson J.H., de Rooij F.W.; "A Gly15Arg mutation in the interleukin-10 gene reduces secretion of interleukin-10 in Crohn disease.,"; Scand. J. Gastroenterol. 38:611-617(2003).; | FT DISULFID; 132 | |
| -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells. | FT CARBOHYD; 134 | |
| -!- SUBUNIT: Homodimer. | FT VARIANT; 15 | |
| -!- SUBCELLULAR LOCALIZATION: Secreted. | FT TURN; 134 | |
| -!- TISSUE SPECIFICITY: Produced by a variety of cell lines, including T cells, macrophages, mast cells and other cell types. | FT TURN; 101 | |
| -!- DISEASE: Defects in IL10 are a cause of susceptibility to Crohn's disease (CD). [MIM:266600], a form of remitting inflammatory bowel disease (IBD). CD may involve any part of the gastrointestinal tract, but most frequently the terminal ileum and colon. Bowel inflammation is transmural and discontinuous. Crohn's disease is commonly classified as autoimmune disease. | FT TURN; 103 | |
| -!- SIMILARITY: Belongs to the IL-10 family. | FT HELIX; 106 | |
| | FT HELIX; 125 | |
| | FT HELIX; 128 | |
| | FT HELIX; 131 | |
| | FT HELIX; 133 | |
| | FT HELIX; 137 | |
| | FT HELIX; 149 | |
| | FT HELIX; 150 | |
| | FT HELIX; 151 | |
| | FT HELIX; 160 | |
| | FT HELIX; 176 | |
| | SO SECRETOR; 178; 1A. 20517 MW. 6825500443377004 CPC64. | |

Query Match 1C.7%; Score 96.5%; DB 1; Length 178;
 Best Local Similarity 22.4%; Pred. No. 0 0.045%; Indels 31; Gaps 6;
 Matches 41; Conservative 33; Mismatches 78; Del 6;
 SUST 11

1 8 TSCLLILAL-LYQGGAAP----ISSHCRIDKSN----FQCPYLTINRTEMLAKDSL 65
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 3 SSALLCCIVLVLIGVRASSGQGTQSENSSTHFPNLPMPLRDRDAFSRKTEFFQMKD--- 59

66 ADNTDYLRLIGEMXENGMSMRSYCYLMKQVINFLTEFLPFQSSDRPQ---YMQEYVPP 121
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 60 --QDNLRLKESLLEDFKGVLGQALSEMIOQYLEEMV-PQENQDPIKAVHNSLGEN 115
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 122 IARISNRISTCHIEGDDHICPENYQKLDTVTKIGESEBIAIGELDIL---LFLMS 173
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 116 LKTLRLRLLRCHRLPCEKNSKRAVEQVNAFNKLQEQGIYKAMSEFDIFINYTEAMTMK 175
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 174 LEN 176

176 IRN 178

10 MARMC STANDARD; PRT; 178 AA.
 Q9JHK7; 26-FEB-2003 (Rel. 41, Created)
 28-FEB-2003 (Rel. 41, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitor factor) (CSIF).
 IL10 OR IL-10.
 Marmota monax (Woodchuck).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 Marmota.
 NCBI_TaxID=9995;

[1] SEQUENCE FROM N.A.

-!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).
 "The woodchuck interleukin-10 gene: cloning and structural analysis", Submitted (JAN-1999) to the EMBL/GenBank/DBJU databases.

-!- SUBUNIT: Homodimer (By similarity).
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- SIMILARITY: Belongs to the IL-10 family.

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EMBL; AF012909; AAF34862.1; -.
 HSSP; P22301; LINR.
 GO; GO:0005756; C: extracellular; ISS.
 GO; GO:0008189; F: apoptosis; sequestering of NF-kappaB; ISS.
 GO; GO:0005141; F: interleukin-10 receptor binding; ISS.
 GO; GO:0006916; F: anti-apoptosis; ISS.
 GO; GO:0006954; F: inflammatory response; ISS.
 GO; GO:00045077; P: negative regulation of interferon-gamma bio-
 GO; GO:0045347; P: negative regulation of MHC class II biosynt. -; ISS.

DR GO; GO:0045019; P: negative regulation of nitric oxide biosynt. -; ISS.
 DR GO; GO:0042130; P: negative regulation of T-cell proliferation; ISS.
 DR GO; GO:0045191; P: regulation of isotype switching; ISS.
 DR GO; GO:0042093; P: helper 2 type immune response; ISS.
 DR GO; GO:0007260; P: tyrosine phosphorylation of STAT protein; ISS.
 DR InterPro; IPR000098; Interleukin-10.
 DR Pfam; PF00726; IL10; 1.
 DR ERANT; PRO1224; INTRALEUKIN10.
 DR PRODOM; PD0003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR SMART; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL; 18 POTENTIAL.
 FT CHAIN; 19 INTERLEUKIN-10.
 FT DISULFID; 30 BY SIMILARITY.
 FT DISULFID; 80 BY SIMILARITY.
 FT CARBOHYD; 134 N-LINKED (GLCNAC. -) (POTENTIAL).
 SQ SEQUENCE 178 AA; 20371 MW; 255B30ACB4CE92A2 CRC64;
 Query Match 10.7%; Score 96.5%; DB 1; Length 178;
 Best Local Similarity 28.2%; Pred. No. 0.045%; Indels 5; Gaps 1.
 Matches 29; Conservative 19; Mismatches 50; Del 6;
 PRT; 178 AA.

Qy 71 DURIGEKEFLPHGVSMSBRCYLMKQVINFLTEFLPFQSSDRPQENQDVFILR---IS 12
 ID IL10_FELCA STANDARD; PRT; 178 AA.
 AC P55029;
 DT 01-OCT-1996 (Rel. 34, Created)
 Db 62 DDMILSESLLEDPEKYLGGQALSMIQYFLVEMV-PQAEQHNSPDYKEHNSLGKEKTLR 12
 Qy 127 NRUSTCHTEGDDLILITQNYVQLKQTKVKGSGEIKAGELDL 169
 DB 121 LRLPERCHRLPCEMSKSKAVQVQDASFSKQBGKLYKAMSEFDI 163
 DB 121 LRLPERCHRLPCEMSKSKAVQVQDASFSKQBGKLYKAMSEFDI 163
 RESULT 12
 IL10_FELCA STANDARD; PRT; 178 AA.
 AC P55029;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DB Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitor factor) (CSIF).
 DE RN
 DE SEQUENCE FROM N.A.
 RA Scott B.M.; O'Reilly K.L.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJU databases.
 CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; U39569; AA81771.1; -.
 CC HSSP; P22301; LINR.
 CC GO; GO:0005576; C: extracellular; ISS.
 CC GO; GO:0005141; F: apoptosis inhibitor activity; ISS.
 CC GO; GO:0005141; F: interleukin-10 receptor binding; ISS.
 CC GO; GO:0005141; F: anti-apoptosis; ISS.
 CC GO; GO:0006916; F: interleukin-10 receptor binding; ISS.
 CC GO; GO:0006954; F: inflammatory response; ISS.
 CC GO; GO:00045077; P: negative regulation of interferon-gamma bio-
 CC GO; GO:0045347; P: negative regulation of MHC class II biosynt. -; ISS.

| RESULT 13 | | Best Local Similarity 23.2%; Pred. No. 0.056; | | Matches 39; Conservative 30; Mismatches 76; Indels 23; Gaps 5 | |
|----------------------------------|--|---|---------|---|--|
| L100 | MACNE | | | | |
| D | _L100_MACNE | STANDARD; | PRT; | 178 AA. | |
| C | PS1497; | | | | |
| T | 01-OCT-1996 | (Rel. 34; Created) | | | |
| T | 01-OCT-1996 | (Rel. 34; Last sequence update) | | | |
| T | 15-DEC-1998 | (Rel. 37; Last annotation update) | | | |
| T | Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF). | | | | |
| N | IL10. | | | | |
| S | Macaca nemestrina (Pig-tailed macaque). | | | | |
| C | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca. | | | | |
| C | NCBI_TaxID=9545; | | | | |
| X | [1] | | | | |
| SEQUENCE FROM N.A. | | | | | |
| C | STRAIN=PT10000; | | | | |
| X | FUNCTION=8603435; PubMed=7561102; | | | | |
| A | Villingen P.-J., Brar S.-S., Mayne A.-E., Chikkala N., Ansari A.-A.; | | | | |
| X | "Comparative sequence analysis of cytokine genes from human and non-human primates." | | | | |
| A | J. Immunol. 155:3946-3954 (1995). | | | | |
| X | -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity). | | | | |
| C | -!- SUBCELLULAR LOCATION: Homodimer (By similarity). | | | | |
| C | -!- SIMILARITY: Belongs to the IL-10 family. | | | | |
| RESULT 14 | | | | | |
| | IL10_BOVIN | | | | |
| | ID _IL10_BOVIN | STANDARD; | | | |
| | AC P43480; | PRT; | 178 AA. | | |
| | DT 01-NOV-1995 | (Rel. 32; Created) | | | |
| | DT 01-NOV-1995 | (Rel. 32; Last sequence update) | | | |
| | DT 15-DEC-1998 | (Rel. 37; Last annotation update) | | | |
| | DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF). | | | | |
| | GN IL10. | | | | |
| | OS Bos taurus (Bovine). | | | | |
| | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovidae; Bovinae; Bos. | | | | |
| | OC NCBI_TaxID=9513; | | | | |
| | [1] | | | | |
| SEQUENCE FROM N.A. TISSUE=Blood; | | | | | |
| RP | STRAIN=Charolais. | | | | |
| RC | MEDLINE=94156210; PubMed=8112615; | | | | |
| RX | Hash S.M., Brown W.C., Rice-Ficht A.C.; | | | | |
| RA | "Characterization of a cDNA encoding bovine interleukin-10. Comparison | | | | |
| RT | between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial | | | | |
| RU | purposes is illegal without permission from the copyright holders." | | | | |

RT of expression in bovine lymphocytes.";

CC Gene 135:257-261 (1994).

CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the IL-10 family.

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CC EMBL: UC0799; P22301; INR.

DR GO: GO:0005576; C:extracellular; ISS.

DR GO: GO:0008189; F:opposite; inhibitor; activity; ISS.

DR GO: GO:0005141; F:interleukin-10 receptor binding; ISS.

DR GO: GO:0006916; P:anti-apoptosis; ISS.

DR GO: GO:0030183; P:B-cell differentiation; ISS.

DR GO: GO:00342100; P:B-cell proliferation; ISS.

DR GO: GO:0027531; P:cytoplasmic sequestering of NF-kappaB; ISS.

DR GO: GO:0030097; P:depoiesis; ISS.

DR GO: GO:0006954; P:inflammatory response; ISS.

DR GO: GO:0045077; P:negative regulation of interleukin-gamma bio.

DR GO: GO:00345347; P:negative regulation of MAC class II biosynt.

DR GO: GO:0042130; P:negative regulation of nitric oxide biosynt.

DR GO: GO:0045019; P:negative regulation of T-cell proliferation; ISS.

DR InterPro: IPR0000098; P:regulation of isotype switching; ISS.

DR InterPro: IPR0000098; P:helper T cell immune response; ISS.

DR Pfam: PF00726; IL10; 1.

DR PRODOM: PR01294; INTERLEUKIN10.

DR SMART: SM00188; IL10; 1.

DR PROSITE: PS00520; INTERLEUKIN10; 1.

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL_1 18 POTENTIAL.

FT CHAIN_1 18 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID_30 126 BY SIMILARITY.

FT DISULFID_80 132 BY SIMILARITY.

FT CARBOHYD_134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD_178 AA; 2041 NM; 3AD6D176DB9D056 CRC54;

SQ SEQUENCE 1.9 SCULLULLVQGGAAAPISSHCRDKSNFQQPYITNRFMELAK-EASTADNNTDVLRIQE 77

Best Local Similarity 24.1%; Score 95; DB 1; Length 178;

Matches 40; Conservative 32; Mismatches 74; Indels 20; Gaps 6;

Db 5 MLLPCLLCYTSNNSALEDNCKFSTLIPNMLRRAFSSVITYFOTRDKLTKLIDK 64

Qy 1.9 SCULLULLVQGGAAAPISSHCRDKSNFQQPYITNRFMELAK-EASTADNNTDVLRIQE 77

Ds 3 SSALLCCFLVFLAASSDASITSSCITHLP-TSLEHMLRBLAAGEAKTEFQM-K 58

Qy 78 KLFHGVSMSSBRCVYLMKOVINFELLEVLPPSDRPPYQMEVVPPIAR-- 124

Ds 59 DQHLSLITIQSLIDDFKTYLGCOALSITQYLYEVM-PQAENHGPDIKEHYNSLGERLK 117

Qy 125 -1SNRLSTCHIESDDLH1QRLNQKLKDVTKKGESGEKAIGELDL 169

Db 118 TIRLRERCHRFLCPNCNSKAVKVKV7SELQERGTVYKAMSSFDI 163

RESULT 15

IL10-TRIVU STANDARD; PRT; 174 AA.

AC 09779;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

Search completed: June 30, 2004, 19:34:35

Job time : 19 secs

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protein - protein search, using sw model

on: June 30, 2004, 19:32:59 ; Search time 41 Seconds
 (without alignments)
 1377.506 Million cell updates/sec

file: US-10-050-552A-2
 effect score: 903
 sequence: 1 MAALQKSVSSFFLGMTHATSC.....EIKAIIGEGLDILFMSLRLNACI 179

string table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 2017041 seqs, 315518202 residues

actual number of hits satisfying chosen parameters: 1017041

maximum DB seq length: 0
 maximum DB seq length: 2000000000

c-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

SPREMBL 25:
 1: sp_archea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_virus:
 16: sp_bacteriap:
 17: sp_archeap:
 18: sp_ciliates:
 19: sp_chloroplast:
 20: sp_endosymbiont:
 21: sp_gut_bacteria:
 22: sp_helminth:
 23: sp_insect:
 24: sp_mite:
 25: sp_nematode:
 26: sp_prokaryote:
 27: sp_rhizobium:
 28: sp_rickettsia:
 29: sp_silicate:
 30: sp_silicate:
 31: sp_silicate:
 32: sp_silicate:
 33: sp_silicate:
 34: sp_silicate:
 35: sp_silicate:
 36: sp_silicate:
 37: sp_silicate:
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 40: sp_silicate:
 41: sp_silicate:
 42: sp_silicate:
 43: sp_silicate:
 44: sp_silicate:
 45: sp_silicate:

base :
 116.5 12.9 175 13 Q7SX60
 111.5 12.3 183 13 Q802T4
 106.5 11.8 178 11 Q80WE8
 106 11.7 181 13 Q7SX82
 104 11.5 177 12 QBUZJ6
 99.5 11.0 171 12 Q9QSLI
 98.5 10.9 178 6 Q8MK99
 97.5 10.8 220 11 Q925J3
 97 10.7 184 13 Q7ZSY8
 96 10.6 180 13 Q7T3II
 95.5 10.6 178 6 Q9TSJ7
 95.5 10.6 181 11 Q9WP8
 95.5 10.6 183 11 Q9WP8
 94 10.4 178 6 Q9TSJ4
 92.5 10.2 131 11 Q9ERG7
 90.5 10.0 103 11 Q88646

pred. No. is the number of results predicted by cbtree to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Query | Score | Match | Length | DB | ID | Description |
|-------|-------|-------|--------|----|--------|-------------------------|
| 1 | 116.5 | 12.9 | 175 | 13 | Q7SX60 | Q7SX60 tetradon r |
| 2 | 111.5 | 12.3 | 183 | 13 | Q802T4 | Q802T4 fugu rubripinnis |
| 3 | 106.5 | 11.8 | 178 | 11 | Q80WE8 | Q80WE8 Peromyscus |
| 4 | 106 | 11.7 | 181 | 13 | Q7SX82 | Q7SX82 tetraodon r |
| 5 | 104 | 11.5 | 177 | 12 | Q8ZJ6 | Q8ZJ6 cercopithicus a |
| 6 | 99.5 | 11.0 | 171 | 12 | Q9QSLI | Q9QSLI herpesvirus |
| 7 | 98.5 | 10.9 | 178 | 6 | Q8MK99 | Q8MK99 saimiri sci |
| 8 | 97.5 | 10.8 | 220 | 11 | Q925J3 | Q925J3 mus musculus |
| 9 | 97 | 10.7 | 184 | 13 | Q7ZSY8 | Q7ZSY8 tetradon r |
| 10 | 96 | 10.6 | 180 | 13 | Q7T3II | Q7T3II Cypripedium c |
| 11 | 95.5 | 10.6 | 178 | 6 | Q9TSJ7 | Q9TSJ7 felis silv |
| 12 | 95.5 | 10.6 | 181 | 11 | Q925J4 | Q925J4 mus musculus |
| 13 | 95.5 | 10.6 | 183 | 11 | Q9WP8 | Q9WP8 ratmus norvegicus |
| 14 | 94 | 10.4 | 178 | 6 | Q9TSJ4 | Q9TSJ4 oryctolagus c |
| 15 | 92.5 | 10.2 | 131 | 11 | Q9ERG7 | Q9ERG7 peromyscus |
| 16 | 90.5 | 10.0 | 103 | 11 | Q88646 | Q88646 marmota mon |

ALIGNMENTS

| RESULT 1 | Q7SX60 | PRELIMINARY; | PRT; | 175 AA. |
|-----------------------|--|---|----------------|-------------|
| ID | Q7SX60 | | | |
| AC | Q7SX60; | | | |
| DT | 01-OCT-2003 | [TREMBURE1. 25, Created] | | |
| DT | 01-OCT-2003 | [TREMBURE1. 25, Last sequence update] | | |
| DT | 01-OCT-2003 | [TREMBURE1. 25, Last annotation update] | | |
| DE | Interleukin-20. | | | |
| DN | IL20. | | | |
| OS | Tetraodon nigroviridis (Green puffer). | | | |
| OC | Metazoa; Chordata; Craniata; Vertebrates; | | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Buteostei; | | | |
| OC | Acanthomorpha; Acanthopterygii; Percomorpha; Tetra- | | | |
| OC | Tetraodontidae; Tetraodontidae; | | | |
| OX | NCBI_TaxID=93883; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Lafaille G., Roest Crollius H., Strange-Thomann N., | | | |
| RA | Monneron D., | | | |
| RA | Moegene K., | | | |
| RT | "Independent expansion of a lineage-specific gene family in vertebrates: The class II cytokine receptors and their ligands in mammals and fish." | | | |
| RT | Submitted: MAY-2003 to the EMBL/GenBank/DBJ database | | | |
| RL | EMBL; AY294557; AAP57414.1; -. | | | |
| DR | EMBL; AY294558; AAP57416.1; -. | | | |
| DR | EMBL; AY294559; AAP57417.1; -. | | | |
| SEQ | SEQUENCE 175 AA; 19838 MW; | DE6FA67E0038E034 CRC | | |
| Query Match | 12.9% | Score 116.5; | DB 13; | |
| Best Local Similarity | 24.9% | Pred. No. 0.0013; | | |
| Matches | 43; | Conservative 30; | Mismatches 85; | Identity 85 |
| Qy | 13 MFTLATSCLLALLV--QGGAAPAPISSHCRDJKSNFQOQY | | | |
| Db | 1 MFTLPSCLLFLCLLCLLBAQSQFVLLVSDS1-SADLOEMH | | | |
| Qy | 70 TDWPLIGKFLFQWMSMSPRCYLNQKVNFPLTBYI----F | | | |
| Db | 58 IGYKLLSKRLMFLFQYDQGRCCFLFLRVLQYFVPSVLSSSH | | | |

| SUMMARIES | | | | | | |
|-----------|-------|-------|-------|--------|--------|------------------------------|
| Query | | | Match | | Length | DB |
| Blt | No. | Score | Match | Length | ID | Description |
| 1 | 116.5 | 12.9 | 175 | 13 | Q75X60 | Q75X60 tetrodotoxin |
| 2 | 111.5 | 12.3 | 183 | 13 | Q82T4 | Q82T4 fugu ruber |
| 3 | 106.5 | 11.8 | 178 | 11 | Q8WE8 | Q8WE8 peromyscus |
| 4 | 106 | 11.7 | 181 | 13 | Q75X82 | Q75X82 tetrodotoxin |
| 5 | 104 | 11.5 | 177 | 12 | Q8UJ6 | Q8UJ6 cercopithecus |
| 6 | 99.5 | 11.6 | 171 | 12 | Q95L1 | Q95L1 herpesvirus |
| 7 | 98.5 | 10.9 | 178 | 6 | Q8MK9 | Q8MK9 saimiri |
| 8 | 97.5 | 10.8 | 220 | 11 | Q92J3 | Q92J3 mus musculus |
| 9 | 97 | 10.7 | 184 | 13 | Q72SY8 | Q72SY8 tetrodotoxin |
| 10 | 96 | 10.6 | 180 | 13 | Q73T11 | Q73T11 cyprinus |
| 11 | 95.5 | 10.6 | 178 | 6 | Q95SJ7 | Q95SJ7 felis silvestris |
| 12 | 95 | 10.6 | 181 | 11 | Q92S4 | Q92S4 mus musculus |
| 13 | 95.5 | 10.6 | 183 | 11 | Q9WP2 | Q9WP2 rattus norvegicus |
| 14 | 94 | 10.4 | 178 | 6 | Q95SJ4 | Q95SJ4 oryctolagus cuniculus |
| 15 | 92.5 | 10.2 | 181 | 11 | Q9ERG7 | Q9ERG7 peromyscus |
| 16 | 90.5 | 10.0 | 103 | 11 | Q88646 | Q88646 marmota flaviventris |

| | | |
|----------|---|---|
| Qy | 1.24 RISNRNLISTCHIEGDLIQRVORLKDITVKGES-GEIKAIGELDDLFMSLR 175 | RT "Genomic organization of the deer mouse interleukin-10 gene."; |
| Db | 1.18 R-KQMIKQKCHCJCEQ-ETQKQVDSLIDAFNKEDEASAKVLAIVGELDIFVQLWQ 168 | RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases. |
| RESULT 2 | | |
| Q80274 | PRELIMINARY; PRT; 183 AA. | DR ENBL; AY251593; AAP1353.1; |
| AC | | DR GO; GO-000576; C:extracellular; IEA. |
| Q80274 | PRELIMINARY; PRT; 183 AA. | DR GO; GO-100525; P:cytokine activity; IEA. |
| AC | | DR InterPro; IPR000098; Interleukin_10. |
| Q80274 | PRELIMINARY; PRT; 183 AA. | DR PFam; PF00726; IL10_1. |
| AC | | DR PRINTS; PRO1294; Interleukin10. |
| DT | 01-JUN-2003 (TREMBLrel. 24; Created) | DR PRODOM; PDD03687; Interleukin_10; 1. |
| DT | 01-JUN-2003 (TREMBLrel. 25; Last sequence update) | DR SMART; SM0018; IL10_1. |
| DT | 01-OCT-2003 (TREMBLrel. 25; Last annotation update) | DR PROSITE; PS00520; INTERLEUKIN_10; 1. |
| DE | Interleukin 10 homologue precursor. | DR SEQUENCE_178 AA; 20504 MW; 270044CIA7E8C1FC CRC64; |
| GN | -IL10; | |
| OS | Fugu rubripes (Japanese pufferfish) (Takifugu rubripes). | Query Match 11.8%; Score 106.5; DB 11; Length 178; |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Best Local Similarity 24.1%; Pred. No. 0 014; |
| OC | Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; | Matches 45; Conservative 34; Mismatches 69; Indels 39; Gaps 8; |
| OC | Tetradontoidea; Tetraodontiformes; | SQ |
| OX | Tetraodontidae; Takifugu. | SEQUENCE_178 AA; 20504 MW; 270044CIA7E8C1FC CRC64; |
| RN | [1] _TAXID=31033; | |
| RP | SEQUENCE FROM N. A. | Query Match 14 GTIATSCILLIALLYVGGAAA-----PISSHCRLLD--KSNEQQPYITNRTM 58 |
| RA | Zou J., Clark M.S., Secomb C.J.; | Best Local Similarity 11.8%; Score 106.5; DB 11; Length 178; |
| RT | *Characterisation, expression and promoter analysis of an interleukin | Matches 45; Conservative 34; Mismatches 69; Indels 39; Gaps 8; |
| RT | 10 homologue in the puffer fish, <i>Fugu rubripes</i> ; | SQ |
| RL | Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases. | SEQUENCE_178 AA; 20504 MW; 270044CIA7E8C1FC CRC64; |
| DR | EMBL; AAC39537; CAD2446.1; | |
| DR | GO; GO:0005576; C:extracellular; IEA. | Db 3 GAAPLICELLLA--EVGASREHTNTQGNNNTHPPVSQTYTLELRAFDQY---KTFPP 55 |
| DR | GO; GO:0005125; P:cytokine activity; IEA. | Qy 59 LAKEASLAHDNNTDVRLLGEKLFHGNMSERCYLMKQVNLNFPELEVLPEQSDFQPYNPQEYV 118 |
| DR | GO; GO:0006955; P:immune response; IEA. | Db 56 QKRD----QLDSTLTDSTMKDFGKSYGLCQALSEMIOQFIVVM-PQAENHGPEIKEH 108 |
| DR | InterPro; IPR00098; Interleukin_10. | Qy 119 VPFIAK---TNSRKLSTCKEGDDELTETQRVAVQKLQDTVTKTGESEITKAIGELDLL---170 |
| DR | PFam; PF00726; IL10_1. | Db 109 LNFGEGKLKTIRRQLQRCHRFPLCPENKSKAVAEQVSKSDENKLQENGTYKAMSSEBDIFINCI 168 |
| DR | PRINTS; PRO1294; Interleukin10. | Qy 171 --FMSLR 175 |
| DR | PRODOM; PDD03687; IL10_1. | Db 169 ENAMTR 175 |
| DR | SMART; SM0018; IL10_1. | |
| DR | Signal. | RESULT 4 |
| FT | | Q7SK82 PRELIMINARY; PRT; 181 AA. |
| SQ | SEQUENCE_183 AA; 21076 MW; 5DCF56678F6B404 CRC64; | ID Q7SK82 |
| FT | 21 POTENTIAL SIGNAL. | AC Q7SK82; |
| FT | 183 AA; 21076 MW; | DT 01-OCT-2003 (TREMBLrel. 25; Created) |
| FT | | DT 01-OCT-2003 (TREMBLrel. 25; Last sequence update) |
| FT | | DB Interleukin-24. |
| FT | | GN IL24. |
| FT | | OS Tetraodon nigroviridis (Green puffer). |
| FT | | OC Buiaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| FT | | CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; |
| FT | | RT *Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT mammals and fish."; |
| FT | | RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
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| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II cytokine receptors and their ligands |
| FT | | RT |
| FT | | RT SEQUENCE FROM N.A. |
| FT | | RA Lutjalla G., Roest Crollius H., Stange-Thomann N., Jaiillon O., |
| FT | | RA Moense K., Monneron D.; |
| FT | | RT "Independent expansion of a lineage-specific gene family in |
| FT | | RT vertebrates: The class II |

| RESULT 5 | | | | | |
|----------|---|--|---------|--|--|
| QY | 132 | CHIEGDDLHQIQRNYQKLKOTVKKIGESEGIKAIGELDLDLLENSLRNACI | 179 | | |
| DB | 127 | CNTI-TRYHDHQHAYKFRQFEEHQHRRRTKALGEVDILFYLQDRCV | 172 | | |
| Q8UZG6 | PRELIMINARY; | PRT; | 177 AA. | | |
| TD | Q8UZG6; | | | | |
| AC | | | | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Created) | | | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Last sequence update) | | | | |
| DT | 01-JUN-2003 (TREMBLrel. 24, Last annotation update) | | | | |
| DB | BCRF1 | | | | |
| CC | Cercopithicine herpesvirus 15. | | | | |
| CC | Herpesviridae | | | | |
| CC | Gammaherpesvirinae | | | | |
| CC | Lymphocryptovirus | | | | |
| OX | NCBI_TaxID=104228; | | | | |
| RN | [1] | N | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RX | MEDLINE=97448062; PubMed=8892933; | | | | |
| RA | Franken M., Devreuge O., Rosenzweig M., Annis B., Kieff E., Wang RT | "Comparative analysis identifies conserved tumor necrosis factor receptor-associated factor 3 binding sites in the human and simian Epstein-Barr virus oncogene LMP1."; | | | |
| RT | BT | J. Virol. 70:7819-7826(1996). | | | |
| RL | RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RX | MEDLINE=9341241; PubMed=10482645; | | | | |
| RA | Rivaialler P., Quirk C., Wang F., | "Strong selective pressure for evolution of an Epstein-Barr virus LMP2B homologue in the rhesus lymphocryptovirus."; | | | |
| RT | RL | J. Virol. 73:8867-8872(1999). | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RX | MEDLINE=030494; PubMed=10846073; | | | | |
| RA | Jiang H., Cho Y.-G., Wang F., | "Structural, functional, and genetic comparison of Epstein-Barr nuclear antigen 3A, 3B, and 3C homologues encoded by the rhesus lymphocryptovirus."; | | | |
| RT | RL | J. Virol. 74:5921-5932(2000). | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RX | MEDLINE=2040453; PubMed=10970361; | | | | |
| RA | Rao P., Jiang H., Wang F., | "Cloning of the rhesus lymphocryptovirus viral capsid antigen and Epstein-Barr virus-encoded small RNA homologues and use in diagnosis of acute and persistent infections."; | | | |
| RT | RL | J. Clin. Microbiol. 38:3219-3225(2000). | | | |
| RN | [5] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RX | MEDLINE=21603573; PubMed=11739708; | | | | |
| RA | Rivaialler P., Jiang H., Cho Y.-G., Quink C., Wang F., | "Complete Nucleotide Sequence of the Rhesus Lymphocryptovirus: Generation for an Epstein-Barr Virus Animal Model."; | | | |
| RT | RL | J. Virol. 76:421-426(2002). | | | |
| RN | [6] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RA | Moghaddam A., Annis B., Wang F., | "Validation of the Rhesus Lymphocryptovirus Animal Model." | | | |
| RT | RL | J. Virol. 71:11997 to the EMBL/GenBank/DBJ databases. | | | |
| RN | [7] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=LCL8664; | | | | |
| RA | Moghaddam A., Annis B., Wang F., | "Validation of the Rhesus Lymphocryptovirus Animal Model." | | | |
| RT | RL | J. Virol. 71:11997 to the EMBL/GenBank/DBJ databases. | | | |
| RN | [8] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |

RT vertebrates: The class II cytokine receptors and their ligands in mammals and fish;"

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ54915; CAD6773; 1.;

DR EMBL; AJ54898; CAD6786; 1.;

DR EMBL; AY294557; CADP5741; 1.;

DR GO; GO:005576; C:extracellular; IEA.

DR SMART; SM00188; IL10; 1.

DR InterPro; IPR00098; Interleukin_1C.

DR PRINTS; PRG1294; INTRILEUKIN10.

DR ProDom; PDC03687; Interleukin_10; 1.

DR Sequence 184 AA; 21024 MW; DC210570PFSAT994 CRC64;

Query Match Score 97; DB 13; Length 184;
Best Local Similarity 21.3%; Pred. No. 0.13; Mismatches 81; Indels 14; Gaps 4;
Matches 35; Conservative 34; Mismatches 81; Indels 14; Gaps 4;

Qy 21 LILLALIVGGAAAPISSHCRUDKSNEQQPY-----ITNPRTMFLAKENASLADNNITDIL1 75
Db 6 LLSVLLLSSSSCAVWCATLNNRCCSFLLEGPARLKVLREYNSNIREYEEANDDIL1 65

Qy 76 GEKLFFGVMSMERCYLMQKVNLFNTSEVL-----FPQSDPFPQYQEVYPFIARISNR 128
Db 66 DQSIYEFKPPFACHYDGLKLYDLSVPLASLYTETDQPLPHEVSIQDILQTE 125

Qy 129 LSTC-HIEGDDLHIIQENVQKLKDTRVKIGSEGEIAKIGBDLFL 171
Db 126 VNNCKHEFACKNQEDMNTLTSAYT-CAMQEKGLFKAMGELDLFL 168

RESULT 10

Q7T3I1 ID Q7T3I1; PRELIMINARY;

AC Q7T3I1; 01-OCT-2003 (TREMBLrel. 25, Created)

A DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Interleukin-10.

GN IL-10.

OS Cyprinus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Cyprinus.

NCBI_TaxID=7962;

RN [1]

RP Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB11078C; ECR76885; 1.;

DR Sequence 180 AA; 20907 MW; 7FE85116831FDB39 CRC64;

Query Match Score 10.6%; DB 13; Length 180;

Best Local Similarity 24.3%; Pred. No. 0.16; Mismatches 26; Indels 16; Gaps 3;

Qy 67 DNNTDVR-LIGEKLPHGVMSERCYLMQKVNLFNTLEVLFPQSDPFPQYQEVYPFIARI 125
Db 57 ESNDDMEPFLDENVQNNINSPYGHVNNEILRYLDTPTAVQDHLHSKPTINSIGN 116

Qy 126 SNRLSTCHIEGDDLHIIQBN-----VQKLKDTRVKIGSEGEIAKIGBDLFL 171
Db 117 FQDLKR-----DMRKCNVYFSQNPLBIASIKNSYKERSVKANGEDLILP 165

RESULT 11

Q9TSU7 ID Q9TSU7; PRELIMINARY;

AC Q9TSU7;

RP Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF235006; ARK5250; 1.

DR MGD; MG1:2135548; IL124.

DR GO; GO:0005576; C:extracellular; IEA.

DR InterPro; IPR00009; Interleukin_10.

DR ProDom; PD003687; Interleukin_10.

DR SMART; SM00188; IL10; 1.

DR PROSITE; PS00520; INTERLEUKIN_10; 1.

DR Sequence 181 AA; 20812 MW; 05CA3872D5D555 CRC64;

Query Match Score 10.6%; DB 11; Length 181;
Best Local Similarity 24.0%; Pred. No. 0.18;

RT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DR Interleukin-10.

GN OS

OC Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Buttheria; Carnivora; Fissipedia; Felidae; Felis.

OC NCBI_TaxID=9685;

RN [1]

RP Sequence FROM N.A.

DR Leutenegger C.M.; Hudler J.B.; Misslin C.; Hoffmann-Lehmann R.; Peter D.;

Dean G.A.; Higgins J.; Pedersen N.C.; Lutz H.

RT "Molecular cloning and expression of feline interleukin-10."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

DR DR HSSP; P2301; 1INR.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005125; F:cytokine activity; IEA.

DR GO; GO:0006855; P:immune response; IEA.

DR InterPro; IPR00098; IL10; 1.

DR Pfam; PF00726; IL10; 1.

DR PRINTS; PRO1194; INTRILEUKIN10.

DR PRODOM; PD003687; Interleukin_10; 1.

DR SMART; SM00188; IL10; 1.

DR PROSITE; PS00520; INTERLEUKIN_10; 1.

DR Sequence 178 AA; 20575 MW; 86AJFB97D9C18D08 CRC64;

Query Match Score 95.5%; DB 6; Length 178;
Best Local Similarity 29.4%; Pred. No. 0.17; Mismatches 35; Indels 5; Gaps 2;

Matches 25; Conservative 20; Mismatches 35; Indels 5; Gaps 2;

Qy 89 CYLMMKVNPLFELVLPQSDPFPQYQEVYPFIAR-----ISNLSTCHIEGDDLHIIQBN 144

Db 80 QALSEMIIQYFLEVM_PQAEENPDIDIKQHVNLSGEKLKTLRRLRCHRFPCENSKV 138

Qy 145 VQKLKDTRVKIGSEGEIKAIGBDLFL 169

Db 139 VEQVKTFSKLQERGVYKAMG3BFDI 163

RESULT 12

Q92584 ID Q92584; PRELIMINARY;

AC Q92584; 01-DBC-2001 (TREMBLrel. 19, Created)

DR 01-DBC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Melanoma differentiation associated gene-7.

GN IL24.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP Sequence FROM N.A.

DR SP129/SwJ;

RA Nadirredi M.T.; Lin J.; Su Z.; Shay J.W.; Huberman E.; Fisher P.B.;

RT "Genomic Structure, Chromosomal Localization and Expression of

RT Melanoma Differentiation Associated Gene-7 (mda-7): Potential

RT Relationship with Cellular Senescence.";

RT Submitted (PB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF235006; ARK5250; 1.

DR MGD; MG1:2135548; IL124.

DR GO; GO:0005576; C:extracellular; IEA.

DR InterPro; IPR00009; Interleukin_10.

DR PRODOM; PD003687; Interleukin_10.

DR SMART; SM00188; IL10; 1.

DR PROSITE; PS00520; INTERLEUKIN_10; 1.

DR Sequence 181 AA; 20812 MW; 05CA3872D5D555 CRC64;

| | | | | | | | | | |
|------------------|--|---|-----|------------|---------|--------|-----|------|--|
| Matches | 42; | Conservative | 28; | Mismatches | 68; | Indels | 37; | Gaps | 8; |
| NCBI_TaxID=9986; | | | | | | | | | |
| QY | 20 | CLINLLI--VQGGNAPPISSKATLDEKSMHQQPVITNTRNFMALKASLADRNNTDVLRI | 75 | | | | | | OX |
| Db | 10 | CLSLTLLWNVPGI-LGQEFPSGSCW--TGSVLPPLWEAFTWVTKNTVQTDITTSIRLL | 67 | | | | | | RN |
| QY | 76 | GEKLFHGVSMSBCYLMQVUNFLTEVXLFQSDRERQPMQEVVPPARIASNRLSTCHTE | 135 | | | | | | XP |
| Db | 68 | KPQFLNVSAGESCVLHSLKEYLNTV-----PKVNTSKIAF--KVLRSFST--LA | 116 | | | | | | SEQUENCE FROM N.A. |
| QY | 136 | GDDLH1QRNVYKLKD-TVVKIGESGE-----IAIGELDLL | 170 | | | | | | RC |
| Db | 117 | NNFIVTMSQLQPSKDNMLPSESAHQRFILLFRRAFKQLDTEVALYKAFGEVDIL | 171 | | | | | | TISSUE=Lymph node; |
| RESULT 13 | | | | | | | | | |
| Q9WVFB | | PRELIMINARY; | | PRT; | 183 AA. | | | | MEDLINE=10843729; |
| AC | Q9WVFB; | | | | | | | | RA |
| DT | 01-NOV-1999 | (TREMBLrel. 12; Created) | | | | | | | Perkins H.D.; van Leeuwen B.H.; Hardy C.M.; Kerr P.J.; |
| DT | 01-JUN-2003 | (TREMBLrel. 24; Last annotation update) | | | | | | | "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the European rabbit (Oryctolagus cuniculus)."; |
| DB | C49a. | | | | | | | | Cytokine 12:55-56 (2000); |
| OS | Rattus norvegicus (Rat). | | | | | | | | EMBL; AF058058; AAC23839.1; -. |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Rattus. NCBI_TaxID=10116; | | | | | | | | HSSP; P22301; LINR. |
| RN | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=Sprague-Dawley; | | | | | | | | |
| RA | MEDLINE=930886; PubMed=110381256; | | | | | | | | |
| RA | Soo C., Shaw M.W., Freynilier B., Longaker M.T., Bertolami C.N., Chiu R., Tieu A., Ting K., | | | | | | | | |
| RA | - Bertolami C.N., Longaker M.T., Chiu R., Tieu A., Ting K., | | | | | | | | |
| RC | "Cutaneous rat wound express c49a, a novel gene with homology to the human melanoma differential gene, mda-7."; | | | | | | | | |
| RL | J. Cell. Biochem. 74:1-10(1999). | | | | | | | | |
| DR | EMBL; AF04774; AA69171.1; -; | | | | | | | | |
| DR | GO: GO:0005576; C:extracellular; IEA. | | | | | | | | |
| DR | GO: GO:0005125; P:immune response; IEA. | | | | | | | | |
| DR | InterPro; IPR00098; Interleukin_10. | | | | | | | | |
| DR | ProDom; PD003687; Interleukin 10. | | | | | | | | |
| DR | PROSITE; PS000520; INTERLEUKIN_10; 1. | | | | | | | | |
| DR | SEQUENCE 183 AA; FFC9A96AFC473B4F CRC64; | | | | | | | | |
| RESULT 14 | | | | | | | | | |
| Q9TSJ4 | | PRELIMINARY; | | PRT; | 178 AA. | | | | NCBI_TaxID=10042; |
| Q9TSJ4 | | | | | | | | | RN |
| DT | 01-MAY-2000 | (TREMBLrel. 13; Created) | | | | | | | SEQUENCE FROM N.A. |
| DT | 01-MAY-2000 | (TREMBLrel. 13; Last sequence update) | | | | | | | RC |
| DT | 01-JUN-2003 | (TREMBLrel. 24; Last annotation update) | | | | | | | RA |
| DB | 127 | NRLSTCHIEGDDLH1QRVYQKLKD-----TVKIG-ESGEIKAIGE | 166 | | | | | | Heribert M.M., Schountz T.-i. |
| DB | 112 | KSFST--LANNELVIMSKLQPSKDNAMPLSDARRFLFHTPKOLDIEVALAKAFGE | 163 | | | | | | TISSUE=Spleen; |
| QY | 167 | LDLIFMSLGN 176 | | | | | | | RT |
| DB | 170 | VDILLAMQN 179 | | | | | | | "Cloning of the deer mouse interferon gamma, interlenkin-10 and tumor necrosis factor genes"; |
| RESULT 15 | | | | | | | | | |
| Q9TSJ4 | | PRELIMINARY; | | PRT; | 131 AA. | | | | GO; GO:0005125; P:cytokine activity; IEA. |
| Q9TSJ4 | | | | | | | | | DR |
| DT | 01-MAY-2000 | (TREMBLrel. 13; Created) | | | | | | | GO; GO:0005576; P:immune response; IEA. |
| DT | 01-MAY-2000 | (TREMBLrel. 13; Last sequence update) | | | | | | | DR |
| DT | 01-JUN-2003 | (TREMBLrel. 24; Last annotation update) | | | | | | | InterPro; IPR000038; Interleukin_10. |
| DB | 128 | IL1IFMSLGN 176 | | | | | | | Pfam; PF00726; IL10; 1. |
| DB | 113 | VDILLAMQN 179 | | | | | | | DR |
| Q9TSJ4 | | PRELIMINARY; | | PRT; | 178 AA. | | | | SMART; SM00188; IL10; 1. |
| Q9TSJ4 | | | | | | | | | DR |
| DT | 01-MAY-2000 | (TREMBLrel. 13; Created) | | | | | | | PROSITE; PS00520; INTERLEUKIN_10; 1. |
| DT | 01-MAY-2000 | (TREMBLrel. 13; Last sequence update) | | | | | | | FT |
| DB | 129 | IL1IFMSLGN 176 | | | | | | | NON_TER |
| DB | 114 | VDILLAMQN 179 | | | | | | | 1 |
| Q9TSJ4 | | PRELIMINARY; | | PRT; | 131 AA. | | | | NON_TER |
| Q9TSJ4 | | | | | | | | | 1 |
| DR | SEQUENCE FROM N.A. | | | | | | | | |
| DR | RC | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | PROSITE; PS005125; P:cytokine activity; IEA. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF00726; IL10; 1. | | | | | | | | |
| DR | PRINTER; PRO1294; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF003687; LINR. | | | | | | | | |
| DR | INTERPRO; IPR000038; INTERLEUKIN_10. | | | | | | | | |
| DR | Pfam; PF007 | | | | | | | | |

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SQ  SEQUENCE  131 AA;  15398 MW;  6EA6EA20CDC0234F CRC64;
Query Match          10.2%;  Score 92.5;  DB 11;  Length 131;
Best Local Similarity 24.4%;  Pred. No. 0.23;
Matches 29;  Conservative 25;  Mismatches 54;  Indels 11;  Gaps 3;
Qy   55 R2PEMLAKERSLADNNNTDVLIGEKLFRHVSMSRVCYLMKVQVANFTLBSVLFPQSDRFQPY 114
Db   19 KCFEQKQD-----QJISILLTDSLMKDKYIGCQASEM1QFVLYVM PQAENNGDE 71
Qy   115 MQRVVPPFAR----TSNRLSTCHIEGDLHIONVOKLKDFTTKIGSGEIKAGELDL 169
Db   72 IKEHNLFGEKLTKLRLQRCHFLPOENKSRAVEQVSDFNKLQENGVYKAMSBEFDI 130

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Search completed: June 30, 2004, 19:36:04
 Job time : 43 secs

| Result No. | Score | Query | Length | DB | ID | Description |
|---------------|-------|-------|--------|----|-------------------|--------------------|
| 1 | 897 | 99.3 | 179 | 4 | US-09-870-574-2 | Sequence 2, Appli |
| 2 | 875 | 96.9 | 179 | 4 | US-09-419-168F-28 | Sequence 28, Appli |
| 3 | 875 | 96.9 | 179 | 4 | US-09-354-243B-28 | Sequence 28, Appli |
| 4 | 718 | 79.5 | 179 | 3 | US-09-178-973B-15 | Sequence 15, Appli |
| 5 | 718 | 79.5 | 179 | 4 | US-09-419-168F-27 | Sequence 27, Appli |
| 6 | 718 | 79.5 | 179 | 4 | US-09-354-243B-27 | Sequence 27, Appli |
| 7 | 714 | 79.1 | 179 | 3 | US-09-178-973B-16 | Sequence 16, Appli |
| 8 | 103 | 11.4 | 170 | 1 | US-09-105C-2 | Sequence 2, Appli |
| 9 | 103 | 11.4 | 170 | 2 | US-09-410-654B-2 | Sequence 2, Appli |
| 10 | 103 | 11.4 | 170 | 2 | US-09-474-851-2 | Sequence 2, Appli |
| 11 | 103 | 11.4 | 170 | 2 | US-08-481-160-2 | Sequence 2, Appli |
| 12 | 103 | 11.4 | 170 | 2 | US-08-934-959-4 | Sequence 4, Appli |
| 13 | 103 | 11.4 | 170 | 3 | US-08-170-113-2 | Sequence 2, Appli |
| 14 | 103 | 11.4 | 170 | 3 | US-08-765-994C-26 | Sequence 26, Appli |
| 15 | 103 | 11.4 | 170 | 3 | US-09-088-797-26 | Sequence 26, Appli |
| 16 | 103 | 11.4 | 170 | 3 | US-08-643-810A-2 | Sequence 2, Appli |
| 17 | 103 | 11.4 | 170 | 4 | US-09-552-613-2 | Sequence 2, Appli |
| 18 | 103 | 11.4 | 170 | 4 | US-09-512-256-26 | Sequence 26, Appli |
| 19 | 98.5 | 10.9 | 154 | 4 | US-09-522-824A-3 | Sequence 3, Appli |
| 20 | 97.5 | 10.8 | 220 | 3 | US-08-884-077-2 | Sequence 2, Appli |
| 21 | 96.5 | 10.7 | 178 | 1 | US-08-270-805C-1 | Sequence 1, Appli |
| 22 | 96.5 | 10.7 | 178 | 2 | US-08-654B-1 | Sequence 1, Appli |
| 23 | 96.5 | 10.7 | 178 | 2 | US-08-474-851-1 | Sequence 1, Appli |
| 24 | 96.5 | 10.7 | 178 | 2 | US-08-481-560-1 | Sequence 1, Appli |
| 25 | 96.5 | 10.7 | 178 | 3 | US-08-934-959-6 | Sequence 6, Appli |
| 26 | 96.5 | 10.7 | 178 | 3 | US-08-170-113-1 | Sequence 1, Appli |
| 27 | 96.5 | 10.7 | 178 | 3 | US-08-765-094C-25 | Sequence 25, Appli |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:27:38 ; Search time 23 Seconds
 (without alignments)
 401.785 Million cell updates/sec

Title: US-10-050-552A-2

Perfect score: 903

Sequence: 1 MAALQKSVSSFLMGLATSC.....EIKAIGELDLMFSLRNACI 179

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/poddata/2/iaa/5A_COMB.pep:
 2: /cgn2_6/podata/2/iaa/5B_COMB.pep:
 3: /cgn2_6/podata/2/iaa/5A_COMB.pep:
 4: /cgn2_6/podata/2/iaa/6B_COMB.pep:
 5: /cgn2_6/podata/2/iaa/PECTUS_COMB.pep:
 6: /cgn2_6/podata/2/iaa/backfile1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
 US-09-870-574-2
 ; Sequence 2, Application US/09870574
 ; Patent No. 6551799
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Austin L.
 ; AGARWAL, Sudeepa
 ; Xie, Ming-Hong
 ; APPLICANT: Maruoka, Eileen M.
 ; APPLICANT: Foster, Jessica S.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEAR ACIDS ENCODING
 ; FILE REFERENCE: P2806-1.US
 ; CURRENT APPLICATION NUMBER: US/09/870,574
 ; CURRENT FILING DATE: 2001-05-30
 ; PRIORITY APPLICATION NUMBER: US 60/169,495
 ; PRIORITY FILING DATE: 1999-12-07
 ; PRIORITY APPLICATION NUMBER: PCT/US00/14042
 ; PRIORITY FILING DATE: 2000-05-22
 ; PRIORITY APPLICATION NUMBER: PCT/US00/23328
 ; SEQ ID NO: 7
 ; LENGTH: 179
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-870-574-2

Query Match 99.3%; Score 897; DB 4; Length 179;
 Best Local Similarity 98.3%; Pred. No. 2.2e-100;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Query Match 99.3%; Score 897; DB 4; Length 179;
 Best Local Similarity 98.3%; Pred. No. 2.2e-100;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGLATSC.....EIKAIGELDLMFSLRNACI 60
 Db 1 MAALQKSVSSFLMGLATSC.....EIKAIGELDLMFSLRNACI 60

Qy 61 KEASLADNTDVRLIGEKLPHGVSMSERCYLMQVINFITLEBVLFQSDRFQYMOEVVP 120
 Db 61 KEASLADNTDVRLIGEKLPHGVSMSERCYLMQVINFITLEBVLFQSDRFQYMOEVVP 120

Qy 121 FIAESNLSTCHIGDDLHQLRNTQKLKDFTYKIGESGETKAIGELDLMFSLRNACI 179
 Db 121 FIAESNLSTCHIGDDLHQLRNTQKLKDFTYKIGESGETKAIGELDLMFSLRNACI 179

RESULT 2
 US-09-419-568F-28
 ; Sequence 28, Application US/09419568F

Patent No. 6331613
 GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
 FILE REFERENCE: LUD 5543.2
 CURRENT APPLICATION NUMBER: US/09/419,568F
 CURRENT FILING DATE: 1998-10-18
 PRIOR APPLICATION NUMBER: US/09/354,243
 PRIOR FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: US/09/178,973
 PRIOR FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 29
 SEQ ID NO: 28
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 US-09-419-568F-28

Query Match 96.9%; Score 875; DB 4; Length 179;
 Best Local Similarity 96.1%; Pred. No. 9.9e-98; 5; Mismatches 2; Indels 0; Gaps 0;
 Matches 172; Conservative 152;

Qy 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60
 Db 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60

Qy 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120
 Db 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120

Qy 121 FLARISNRSLSTCHIEGDDLHITQRNVQKLDTVKRGESGEIKAGELDILFMSLRNACI 179
 Db 121 FLARISNRSLSTCHIEGDDLHITQRNVQKLDTVKRGESGEIKAGELDILFMSLRNACI 179

RESULT 3
 US-09-354-243B-28
 Sequence 28; Application US/09/54243B
 Patent No. 6359117

GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
 FILE REFERENCE: LUD 5543.1
 CURRENT APPLICATION NUMBER: US/09/354,243B
 CURRENT FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: US/09/178,973
 PRIOR FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 29
 SEQ ID NO: 28
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 US-09-354-243B-28

Query Match 96.9%; Score 875; DB 4; Length 179;
 Best Local Similarity 96.1%; Pred. No. 9.9e-98; 5; Mismatches 2; Indels 0; Gaps 0;
 Matches 172; Conservative 152;

Qy 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60
 Db 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60

Qy 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120
 Db 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120

RESULT 4
 US-09-419-973B-27
 Sequence 15; Application US/09/178973B
 Patent No. 6274710
 GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
 FILE REFERENCE: LUD 5543
 CURRENT APPLICATION NUMBER: US/09/178,973B
 NUMBER OF SEQ ID NOS: 17
 SEQ ID NO: 15
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 US-09-178-973B-15

Query Match 79.5%; Score 718; DB 3; Length 179;
 Best Local Similarity 76.5%; Pred. No. 9.5e-79; 20; Mismatches 20; Indels 0; Gaps 0;
 Matches 137; Conservative 20;

Qy 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60
 Db 1 MAVLQKMSMSLMLGTLAASCLLTAALMAQANALPVNTRCKLVEISNFOQQYTINRTMFLA 60

Qy 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120
 Db 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120

Qy 121 FLARISNRSLSTCHIEGDDLHITQRNVQKLDTVKRGESGEIKAGELDILFMSLRNACI 179
 Db 121 FLTRKLSNQLSSCHISGDDONIQKRNVRKLTVKRGESGEIKAGELDILFMSLRNACI 179

RESULT 5
 US-09-419-568F-27
 Sequence 27; Application US/09/19568F
 Patent No. 6313613
 GENERAL INFORMATION:
 APPLICANT: Dumoutier, Laure
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
 FILE REFERENCE: LUD 5543.2
 CURRENT APPLICATION NUMBER: US/09/419,568F
 CURRENT FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: US/09/354,243
 PRIOR FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: US/09/178,973
 PRIOR FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 29
 SEQ ID NO: 27
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 US-09-419-568F-27

Query Match 79.5%; Score 718; DB 4; Length 179;
 Best Local Similarity 76.5%; Pred. No. 9.5e-79; 22; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60
 Db 1 MAALQKSVSSFLMGLTATSCLLLLVQGAAPISHSQCRDKSNEQQPYITNRTMFLA 60

Qy 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120
 Db 61 KEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLFNFTLPPQDRQPMQEVYP 120

RESULT 6
 US-09-354-243B-27
 i Sequence 27 Application US/09354243B
 i Patent No. 559117
 i GENERAL INFORMATION:
 i i APPLICANT: Dumoutier, Laure
 i i APPLICANT: Louhed, Jamila
 i i APPLICANT: Renaud, Jean-Christophe
 i i TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factor
 i i TITLE OF INVENTION: (TIFs)
 i i TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
 i i FILE REFERENCE: LUD 5543.1
 i i CURRENT APPLICATION NUMBER: US/09/354,243B
 i i CURRENT FILING DATE: 1999-07-16
 i i PRIOR APPLICATION NUMBER: US09/178,973
 i i PRIOR FILING DATE: 1998-10-26
 i i NUMBER OF SEQ ID NOS: 29
 i i SEQ ID NO 27
 i i LENGTH: 179
 i i TYPE: PRT
 i i ORGANISM: Mus musculus
 i i FEATUE:
 i i US-09-354-243B-27

Query Match 1 MAALOKSVSSPELMGLATSCILLALLVQGAAAPISSCHRLDKSNFQQYITINRTFMLA 60
 Best Local Similarity 97.5%; Pred. No. 9.5e-79; 0 Mismatches 20; Indels 0; Gaps 0;
 Matches 137; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 MAALOKSVSSPELMGLATSCILLALLVQGAAAPISSCHRLDKSNFQQYITINRTFMLA 60
 Db 1 MAVLOKSMSSPELMGLAASCILLIWAQANALPNTRKCLEVNLKQVLTNFITLVEVLFPQSDFQPMQEYVP 120
 Qy 61 KEASLADNNTDVRLIGEKLFHGVSISERCYLMKQVLTNFITLVEVLFPQSDFQPMQEYVP 120
 Db 61 KEASLADNNTDVRLIGEKLFHGVSISERCYLMKQVLTNFITLVEVLFPQSDFQPMQEYVP 120
 Qy 121 FIARISNRSLSTCHIGEDDLHTQNRVYQKLDTIVKIGESEGETKAIGELDLMFMSLRNACI 179
 Db 121 FLTKLSNQLSSCHISSEDDQNTQKVRRLKETVCKIGESEGETKAIGELDLMFMSLRNACI 179
 Qy 121 FIARISNRSLSTCHIGEDDLHTQNRVYQKLDTIVKIGESEGETKAIGELDLMFMSLRNACI 179
 Db 121 FLTKLSNQLSSCHISSEDDQNTQKVRRLKETVCKIGESEGETKAIGELDLMFMSLRNACI 179

RESULT 7
 US-09-178-973B-16
 i Sequence 16 Application US/09178973B
 i Patent No. 5274710
 i GENERAL INFORMATION:
 i i APPLICANT: Dumoutier, Laure
 i i APPLICANT: Louhed, Jamila
 i i APPLICANT: Renaud, Jean-Christophe
 i i TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factor
 i i TITLE OF INVENTION: (TIFs)
 i i TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
 i i FILE REFERENCE: LUD 5543
 i i CURRENT APPLICATION NUMBER: US/09/178,973B
 i i CURRENT FILING DATE: 1998-10-26
 i i NUMBER OF SEQ ID NOS: 17
 i i SEQ ID NO 16
 i i LENGTH: 179
 i i TYPE: PRT

ORGANISM: Mus musculus
 US-09-178-973B-16
 Query Match 1 MAALOKSVSSPELMGLATSCILLALLVQGAAAPISSCHRLDKSNFQQYITINRTFMLA 60
 Best Local Similarity 79.1%; Pred. No. 2.9e-78; 23; Mismatches 20; Indels 0; Gaps 0;
 Matches 136; Conservative 23; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 MAALOKSVSSPELMGLATSCILLALLVQGAAAPISSCHRLDKSNFQQYITINRTFMLA 60
 Db 1 MAVLOKSMSSPELMGLAASCILLIWAQANALPNTRKCLEVNLKQVLTNFITLVEVLFPQSDFQPMQEYVP 120
 Qy 61 KEASLADNNTDVRLIGEKLFHGVSISERCYLMKQVLTNFITLVEVLFPQSDFQPMQEYVP 120
 Db 61 KEASLADNNTDVRLIGEKLFHGVSISERCYLMKQVLTNFITLVEVLFPQSDFQPMQEYVP 120
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 Db 121 FLTKLSNQLSSCHISSEDDQNTQKVRRLKETVCKIGESEGETKAIGELDLMFMSLRNACI 179
 Qy 121 FIARISNRSLSTCHIGEDDLHTQNRVYQKLDTIVKIGESEGETKAIGELDLMFMSLRNACI 179
 Db 121 FLTKLSNQLSSCHISSEDDQNTQKVRRLKETVCKIGESEGETKAIGELDLMFMSLRNACI 179
 RESULT 8
 US-08-270-805C-2
 i Sequence 2 Application US/08270805C
 i Patent No. 5776451
 i GENERAL INFORMATION:
 i i APPLICANT: Di-Hwei HSU
 i i APPLICANT: Kevin K. Moore
 i i APPLICANT: Hergen Spits
 i i TITLE OF INVENTION: Use of Interleukin-10 in Adoptive Immunotherapy
 i i TITLE OF INVENTION: Use of Interleukin-10 in Adoptive Immunotherapy
 i i NUMBER OF SEQUENCES: 25
 i i CORRESPONDENCE ADDRESS:
 i i ADDRESSEE: Schering-Plough Corporation
 i i STREET: 2000 Galloping Hill Road
 i i CITY: Kenilworth
 i i STATE: New Jersey
 i i COUNTRY: USA
 i i ZIP: 07033
 i i COMPUTER READABLE FORM:
 i i MEDIUM TYPE: Floppy disk
 i i COMPUTER: Macintosh
 i i OPERATING SYSTEM: 7.5.3
 i i CURRENT APPLICATION DATA:
 i i APPLICATION NUMBER: US/08/270,805C
 i i FILING DATE: 05-July-1994
 i i CLASSIFICATION: 424
 i i PRIORITY APPLICATION DATA:
 i i APPLICATION NUMBER: US 07/995,564
 i i FILING DATE: 23-Dec-1992
 i i APPLICATION NUMBER: US 07/830,493
 i i FILING DATE: 04-Feb-1992
 i i APPLICATION NUMBER: US 07/641,342
 i i FILING DATE: 16-Jan-1991
 i i ATTORNEY/AGENT INFORMATION:
 i i NAME: Follike, Cynthia L.
 i i REGISTRATION NUMBER: 32,364
 i i TELECOMMUNICATION INFORMATION:
 i i TELEPHONE: 908-298-2987
 i i TELEFAX: 908-298-5388
 i i INFORMATION FOR SEQ ID NO: 2:
 i i SEQUENCE CHARACTERISTICS:
 i i LENGTH: 170 amino acids
 i i TYPE: amino acid
 i i STRANDEDNESS: single
 i i TOPOLOGY: linear
 i i MOLECULE TYPE: Peptide
 i i US-08-270-805C-2

Qy 20 CLLIAALYQGGAAPISSHCRDKNSFQQ-----PYITNRTEMLAKEASLADNNTV 72
 Db 11 CLVLYLAPCGG----TDQC----DNPQMLRDRFASRVKTCFFQTKD-----EVIN 56

Qy 73 RLIBGEKLFHGVSMSERCYLMKQVLFNFTLEEVLFQPSDFQPMQEVVPPFAR---ISNR 128
 Db 57 LLIKESELDFKGYLGCCALSEMQFYLEVM-PQANQDPEAKDHNSLGENKLRLR 115

Qy 129 LSTCHIEGDDLHICRNVORKLKDVKKIGBSEGEIAIGRIDE 169
 Db 116 LRRCHRFLPCENSKSAVEQIKNAFNKLOEGKTYKAMSEFDI 156

Db 57 LLIKESELDFKGYLGCCALSEMQFYLEVM-PQANQDPEAKDHNSLGENKLRLR 115

RESULT 10
 US-08-474-851-2
 ; Sequence 2, Application US/08474851
 ; Patent No. 5837232

GENERAL INFORMATION:
 ; APPLICANT: Rene de Waal Malefyt
 ; APPLICANT: Di-Wei Hsu
 ; APPLICANT: Anne O'Garra
 ; APPLICANT: Hergen Spits
 ; TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat
 ; TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schering-Plough Corporation
 ; STREET: 2000 Galloping Hill Road
 ; CITY: Kenilworth
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07033
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: 7.5.3
 ; SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,851
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/410,654
 ; FILING DATE: 24-MAR-1995
 ; APPLICATION NUMBER: US/08/229,854
 ; FILING DATE: 19-APR-1994
 ; APPLICATION NUMBER: 08/410,654
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US/08/229,854
 ; FILING DATE: 19-APR-1994
 ; APPLICATION NUMBER: 08/410,654
 ; FILING DATE: 05-AUG-1992
 ; APPLICATION NUMBER: 08/410,654
 ; FILING DATE: 05-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foulke, Cynthia L.
 ; REGISTRATION NUMBER: 32,364
 ; REFERENCE/DOCKET NUMBER: DX0221KQ1GD
 ; TELEPHONE: 908-298-2987
 ; TELEFAX: 908-298-2987
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; US-08-474-851-2

Query Match 11.4%; Score 103; DB 2; Length 170;
 Best Local Similarity 24.8%; Pred. No. 0.0002; Mismatches 27; Indels 26; Gaps 6;

Qy 20 CLVLYLAPCGG----DNPQMLRDRFASRVKTCFFQTKD-----PYITNRTEMLAKEASLADNNTV 72
 Db 11 CLVLYLAPCGG----TDQC----DNPQMLRDRFASRVKTCFFQTKD-----EVIN 56

Qy 73 RLIBGEKLFHGVSMSERCYLMKQVLFNFTLEEVLFQPSDFQPMQEVVPPFAR---ISNR 128
 Db 57 LLIKESELDFKGYLGCCALSEMQFYLEVM-PQANQDPEAKDHNSLGENKLRLR 115

Qy 20 CLVLYLAPCGG----DNPQMLRDRFASRVKTCFFQTKD-----PYITNRTEMLAKEASLADNNTV 72
 Db 11 CLVLYLAPCGG----TDQC----DNPQMLRDRFASRVKTCFFQTKD-----EVIN 56

Qy 73 RLIBGEKLFHGVSMSERCYLMKQVLFNFTLEEVLFQPSDFQPMQEVVPPFAR---ISNR 128
 Db 57 LLIKESELDFKGYLGCCALSEMQFYLEVM-PQANQDPEAKDHNSLGENKLRLR 115

| | | |
|-----------|---|--|
| Qy | 129 | LSTCHIEGDDLHQIYQKLUKDVTYKIGSGEIKAGIELDL 169 |
| Qy | 116 | RRCHRFLPCENSKRAVEQIKAFLQNLQEKGIYKAMSEFDFI 156 |
| Db | 116 | RRCHRFLPCENSKRAVEQIKAFLQNLQEKGIYKAMSEFDFI 156 |
| RESULT 11 | | |
| | US-08-481-560-2 | |
| | Sequence 2, Application US/08481560 | |
| | Patent No. 5837293 | |
| | GENERAL INFORMATION: | |
| | APPLICANT: Rene de Waal Malefyt | |
| | APPLICANT: Di-Hwei Hsu | |
| | APPLICANT: Andre O'Garra | |
| | APPLICANT: Hergen Spits | |
| | TITLE OF INVENTION: Use of Interleukin-10 to Modulate Inflammation or T-Cell Mediated Immune Function | |
| | TITLE OF INVENTION: Inflammation or T-Cell Mediated Immune Function | |
| | NUMBER OF SEQUENCES: 61 | |
| | CORRESPONDENCE ADDRESS: | |
| | ADDRESSEE: Schering-Plough Corporation | |
| | STREET: 2000 Galloping Hill Road | |
| | CITY: Kenilworth | |
| | STATE: New Jersey | |
| | COUNTRY: USA | |
| | ZIP: 07033 | |
| | COMPUTER READABLE FORM: | |
| | MEDIA TYPE: Floppy disk | |
| | COMPUTER: Macintosh | |
| | OPERATING SYSTEM: 1.5.3 | |
| | SOFTWARE: Microsoft Word 6.0 | |
| | CURRENT APPLICATION DATA: | |
| | APPLICATION NUMBER: US/08/481,560 | |
| | APPLICATION NUMBER: US/08/481,560 | |
| | FILING DATE: 07-JUN-1995 | |
| | CLASSIFICATION: 424 | |
| | PRIOR APPLICATION DATA: | |
| | APPLICATION NUMBER: 08/410,654 | |
| | FILING DATE: 24-MAR-1995 | |
| | APPLICATION NUMBER: US/08/229,954 | |
| | FILING DATE: 19-APR-1994 | |
| | APPLICATION NUMBER: US/07/926,853 | |
| | FILING DATE: 06-AUG-1992 | |
| | APPLICATION NUMBER: US/07/742,129 | |
| | FILING DATE: 06-AUG-1991 | |
| | ATTORNEY/AGENT INFORMATION: | |
| | NAME: Foulke, Cynthia L. | |
| | REGISTRATION NUMBER: 32,364 | |
| | REFERENCE/DOCKET NUMBER: DX0221KQ1GC | |
| | TELECOMMUNICATION INFORMATION: | |
| | TELEPHONE: 908-298-2987 | |
| | TELEFAX: 908-298-5388 | |
| | SEQUENCE FOR SEQ ID NO: 2: | |
| | SEQUENCE CHARACTERISTICS: | |
| | LENGTH: 170 amino acids | |
| | TYPE: amino acid | |
| | STRANDEDNESS: single | |
| | TOPOLOGY: linear | |
| | MOLECULE TYPE: peptide | |
| | US-08-481-560-2 | |
| Query | 20 | CILILILIVQGGAAAAPLSSHCRDKSNFQQ-----PYITNRTEN |
| Query | 11 | CLVLLVLAPECGG-----TDOC-----DNFQMLRDLRDFASRYKTFP |
| Db | 11 | CLVLLVLAPECGG-----TDOC-----DNFQMLRDLRDFASRYKTFP |
| Query | 73 | RLIGEKLFLHGVSMSERCYLMKQVNLTFLEEVLFQSDRFPQYMQET |
| Db | 57 | LJLKESLLEDFKGGLQALSEMTOFYLEVM-POAENQDPFKEAKCBLDL 169 |
| Query | 73 | LJLKESLLEDFKGGLQALSEMTOFYLEVM-POAENQDPFKEAKCBLDL 169 |

RESULT 12
 US-08-934-959-4
 ; Sequence 4, Application US/0834959
 ; Patent No. 5989867
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappe, Andrea
 ; APPLICANT: Fickenscher, Helmut
 ; APPLICANT: Fleckenstein, Bernhard
 ; TITLE OR INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901, California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,959
 ; FILING DATE: 22-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/027,368
 ; FILING DATE: 23-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/MOCKET NUMBER: DX0644K
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-852-1996
 ; TELEFAX: 650-496-1200
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; US-08-934-959-4

Query Match Score 103; DB 2; Length 11.4%; Best Local Similarity 24.8%; Pred. No. 0.0002; Mismatches 68; Index Matches 40; Conservative 27; Indel 13

Qy 20 CELLULLARYGGAAPISSHCRUDKNSFCQ----PYITDRTFPI
 Db 11 CLVLYLAPCGG----TDOC----DNPQMLRDLDRFSRVKTF
 Qy 73 RLIGEKLFLHGVSMSERCYLMKVOVNTFLKEVLFVPSQDRFQPYQWE
 Db 57 ILLKESLLEBDPKGYGQCALEMSITQFYLEEVM--POAENQDPEAKD
 Qy 129 LSTCHIEGDDLHIIORNVQQLKDTVVKIGSGEKAIGELDL 169
 Db 116 LRRCRELPCENSKKAVEQIKNAFNKLQEQKGYKAMSEBFEDI 156

RESULT 13
 US-08-170-113-2
 ; Sequence 2, Application US/08170113
 ; Patent No. 6106823
 ; GENERAL INFORMATION:
 ; APPLICANT: Vieira, Paulo J.
 ; APPLICANT: Moore, Kevin W.
 ; APPLICANT: De Waal Malefyt, Rene

APPLICANT: de Vries, Jan E.
 APPLICANT: Fluckinger, Anne-Catherine
 APPLICANT: Banchereau, Jacques
 TITLE OF INVENTION: TREATMENT OF NEOPLASTIC DISEASE WITH
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNA Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-11C4

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/170,113
 FILING DATE: 17-DEC-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/933,419
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/091,333
 FILING DATE: 12-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/020,018
 FILING DATE: 17-FEB-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/830,496
 FILING DATE: 04-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/641,347
 FILING DATE: 16-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0116Q1KX
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-3196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-170-113-2

Query Match 20 CLVLLALVQGGAAPISSHCRLLDKSNFQQ- Score 103; DB 3; Length 170;
 Best Local Similarity 24.8%; Pred. No. 0.0002; Indels 27; Mismatches 27; Gaps 6;
 Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;

Qy 20 CLVLLALVQGGAAPISSHCRLLDKSNFQQ- Score 103; DB 3; Length 170;
 Db 11 CLVLLALVQGGAAPISSHCRLLDKSNFQQ- Score 103; DB 3; Length 170;
 Db 11 CLVLLALVQGGAAPISSHCRLLDKSNFQQ- Score 103; DB 3; Length 170;
 Db 11 CLVLLALVQGGAAPISSHCRLLDKSNFQQ- Score 103; DB 3; Length 170;

Query Match 73 BLIGEKLFLFGVMSMSRCLYMKQVINFITLEEVLPQSDRFQPMQEYVPPFAR- Score 128; DB 56
 Best Local Similarity 24.8%; Pred. No. 0.0002; Indels 26; Mismatches 27; Gaps 6;
 Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;

Qy 73 BLIGEKLFLFGVMSMSRCLYMKQVINFITLEEVLPQSDRFQPMQEYVPPFAR- Score 128; DB 56
 Db 57 LLKESLLEDFKGVLGQALSEMIOFYLEVM-PQAENQDPEAKHVNLSGENKLTLRLR 115

Query Match 129 LSTCHIEGDLHIVQVNLQKTDYKIGESEIKAGEGLDL 169
 Best Local Similarity 24.8%; Pred. No. 0.0002; Indels 26; Mismatches 27; Gaps 6;
 Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;

Qy 129 LSTCHIEGDLHIVQVNLQKTDYKIGESEIKAGEGLDL 169
 Db 116 LRRCHRLPCENSKSKAVEQ1KNAFKLQEGKJYXAMSEFDI 156

RESULT 15 US-08-170-113-2
 Sequence 26, Application US/09082797
 Patent No. 6168791

GENERAL INFORMATION:
 APPLICANT: GRONHOJ LARSEN, Christian
 APPLICANT: GESSER, Borbala
 TITLE OF INVENTION: IMMUNOMODULATORS
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEMARK, P.L.L.C.
 STREET: 419 Seventh Street N.W., Suite 300
 CITY: Washington

STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/082,797
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/765,094
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DK 0800/94
 FILING DATE: 05-JUL-1994
 ATTORNEY / AGENT INFORMATION:
 NAME: COOPER, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: GRONEHOJ-LARSEN=1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 737-5528
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-082-797-26

Query Match 11.4%; Score 103; DB 3; Length 170;
 Best Local Similarity 24.8%; Pred. No. 0.0002; Mismatches 6;
 Matches 40; Conservative 27; Indels 26; Gaps 6;
 Qy 20 CMLIALWQGGAAPPISSHCRLDKSNFQQ-----PYVITKRTFMLAKEASLADNNNTDV 72
 Db 11 CLVILLYAPECGG-----TDQC-----DNFQMLRDLRDAFSRVCTTFQTKD-----EVDN 56
 Qy 73 RLIGEKLPHGVSMSERCYLMKOVNFTLLEVLPQSDRQPMTQEVVTPFIAAR---ISMR 128
 Db 57 LIIKESLLEDFKSYLGCQALSENTOFYLEVM-POAENQDPEAKDHNSGENLKTLR 115
 Qy 129 LSTCHIEGDLHQANVYQRLKDVTKIGSGETKAIGBDL 169
 Db 116 LRRCHRFELCENKSKAVEQKNAFQNLQEKGYKAMSEFDI 156

Search completed: June 30, 2004, 19:34:04
 Job time : 24 secs

Db 112 LKTLRLRLRRCHQFLPCENKSKAVERVYKSAFSKLQERGVYKAMGBRDI 159

RESULT 5

JN0475
interleukin-10 precursor - rat
N:Alternate names: cytokine synthesis inhibitory factor
C:Species: Rattus norvegicus (Norway rat)
C:Accession: JN0475; JCI357; S36021
R:Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.
Biochem. Biophys. Res. Commun. 192, 452-458, 1992
A:Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and
A:Reference number: JN0475
A:Status: nucleic acid sequence not shown
A:Residues: 1-178 <PEN>
R:Goodman, R.E.; Oblik, J.; Bell, R.G.
Biochem. Biophys. Res. Commun. 189, 1-7, 1992
A:Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from b
A:Reference number: JCI357; MUID:93080542; PMID:1280414
A:Accession: JCI357
A:Molecule type: mRNA
A:Residues: 1, 'P', 3-64, 'L', 66-178 <GOO>
A:Cross-references: GB:J02926; NTID:9204903; PIDN:AAA41425.1; PID:9204904
R:Feng, L.
A:Submitted to the EMBL Data Library, July 1991
A:Accession: S36021
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-178 <FE2>
,

A:Cross-references: EMBL:X6075; PIDN:CAA43090.1; PID:9296621
C:Keywords: cytokine; glycoprotein; lymphokine; T-cell
P:1-18/Domain: signal sequence #status predicted <SIG>
,

P:19-178/Domain: interleukin-10 #status predicted <MAT>

P:114/Domain: binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.6%; Score 86.5; DB: 2; Length 178;
Best Local Similarity 24.3%; Pred. No. 0.89; Gaps 9;
Matches 43; Conservative 33; Mismatches 66; Indels 37; Gaps 9;
C:Species: interleukin-10
C:Accession: S36021
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* subsp. *lactis*
A:Reference number: AB0066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <STO>
A:Cross-references: GB:AB005176; PID:91273351; PID:AAK04570.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pi137

A:Cross-references: GB:AL590842; PIDN:CA89394.1; PID:91597863C; GSPDB:GN00175
C:Genetics:
A:Gene: YP00537
C:Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog
Query Match 9.5%; Score 85.5; DB: 2; Length 601;
Best Local Similarity 25.4%; Pred. No. 4.8; Gaps 9;
Matches 44; Conservative 27; Mismatches 61; Indels 41; Gaps 9;
C:Species: Picca glauca (white spruce)
C:Accession: T09251
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
R:Dong, J.Z.; Dunstan, D.I.
A:Accession: T09251
A:Title: Cloning and characterization of 6 novel plant embryogenesis-associated
A:Reference number: Z116629
A:Accession: T09251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <DON>
A:Cross-references: EMBL:L47671; NID:91350511; PID:91350512
C:Genetics:
C:Superfamily: white spruce late embryonic abundant protein BMB35
C:Species: Lactococcus lactis subsp. *lactis*
C:Accession: H86683
R:Boletin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarie, K.; Weissenbach, J.; Ehr
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*
A:Reference number: AB06225; MUID:21235186; PMID:11337471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <STO>
A:Cross-references: GB:AB005176; PID:91273351; PID:AAK04570.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pi137

A:Cross-references: GB:AL590842; PIDN:CA89394.1; PID:91597863C; GSPDB:GN00175
C:Genetics:
A:Gene: YP00537
C:Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog
Query Match 9.5%; Score 85.5%; DB: 2; Length 601;
Best Local Similarity 25.4%; Pred. No. 4.8; Gaps 9;
Matches 44; Conservative 27; Mismatches 61; Indels 41; Gaps 9;
C:Species: Picca glauca (white spruce)
C:Accession: T09251
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
R:Dong, J.Z.; Dunstan, D.I.
A:Accession: T09251
A:Title: Cloning and characterization of 6 novel plant embryogenesis-associated
A:Reference number: Z116629
A:Accession: T09251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <DON>
A:Cross-references: EMBL:L47671; NID:91350511; PID:91350512
C:Genetics:
C:Superfamily: white spruce late embryonic abundant protein BMB35
C:Species: Lactococcus lactis subsp. *lactis*
C:Accession: H86683
R:Boletin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarie, K.; Weissenbach, J.; Ehr
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*
A:Reference number: AB06225; MUID:21235186; PMID:11337471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <STO>
A:Cross-references: GB:AB005176; PID:91273351; PID:AAK04570.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pi137

A:Cross-references: GB:AL590842; PIDN:CA89394.1; PID:91597863C; GSPDB:GN00175
C:Genetics:
A:Gene: YP00537
C:Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog
Query Match 9.5%; Score 85.5%; DB: 2; Length 601;
Best Local Similarity 25.4%; Pred. No. 4.8; Gaps 9;
Matches 44; Conservative 27; Mismatches 61; Indels 41; Gaps 9;
C:Species: Picca glauca (white spruce)
C:Accession: T09251
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
R:Dong, J.Z.; Dunstan, D.I.
A:Accession: T09251
A:Title: Cloning and characterization of 6 novel plant embryogenesis-associated
A:Reference number: Z116629
A:Accession: T09251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <DON>
A:Cross-references: EMBL:L47671; NID:91350511; PID:91350512
C:Genetics:
C:Superfamily: white spruce late embryonic abundant protein BMB35
C:Species: Lactococcus lactis subsp. *lactis*
C:Accession: H86683
R:Boletin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarie, K.; Weissenbach, J.; Ehr
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis*
A:Reference number: AB06225; MUID:21235186; PMID:11337471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <STO>
A:Cross-references: GB:AB005176; PID:91273351; PID:AAK04570.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pi137

Query Match 8.8%: Score 79.5; DB 2; Length 688;
 Best Local Similarity 22.3%; Pred. No. 21;
 Matches 42; Conservative 27; Mismatches 62; Indels 57; Gaps 8;
 A:Accession: S50608
 A;Molecule type: DNA
 A;Cross-references: 1-1391 <DB>
 C;Species: EMBL:U18839; NID:9603313; PID:AAH64650.1; MIPS:YER1
 C;Genetics:
 A;Gene: SGD:NP157
 A;Cross-references: SGD:S0000907; MIPS:YER105C
 A;Map position: 5R

Qy 17 ATSCLLLALLYQGGAAPIS--SHCRUDKSNFQOPYTNRTPMALKASL----- 65
 Db 129 ASAALFFAHTI-----APIKSYSACRI--ARMDNNEFTINPSASLLNSDLDLFSVSGTK 180

Qy 66 ADNTTDVPLIGEKU-----PHGVSMSERCYLMKQVNLNFTEVLPFQPSDF- 111
 Db 181 SLNMIEMERSLGQNLNALBPLMDEALELAQKSRETCALYEEAFTPYNELLFKEGSGIV 240

Qy 112 -----QPMQEVYPPFIAISNRSLSTCHLEGDDHIIQRTWQKLDTVKIGESCR 161
 Db 241 LNRLLQDQKNCYFDEIILK-----GTESSALSERENY--PCEVAKKTSBHS 286

Qy 162 KATGELD 169
 Db 287 FSLEETEL 294

RESULT 13

E64671
 Polynucleotide phosphotriolase - *Helicobacter pylori* (strain 26695)
 C;Species: *Helicobacter pylori*
 C;Date: 09-Aug-1997 #text_change 09-Aug-1997 #text_revision 09-Aug-1997
 C;Accession: E64671
 R;Tomb, J. F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna,
 J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
 Nature 388, 539-547, 1997
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karplus, P.D.; Smith, H.O.; Fraser, C.
 A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*. C.
 A;Reference number: A64520; PMID:925185
 A;Accession: E64671
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-688 <TOMs>
 A;Cross-references: GB:AB000627; GB:AB000511; PID:9314373; PID:9231437
 C;Superfamily: polyribonucleotide nucleotidyltransferase

Query Match 8.8%: Score 79.5; DB 2; Length 688;
 Best Local Similarity 21.4%; Pred. No. 21;
 Matches 39; Conservative 28; Mismatches 60; Indels 55; Gaps 7;
 A:Accession: S50608
 A;Molecule type: DNA
 A;Cross-references: 1-1391 <DB>
 C;Species: Saccharomyces cerevisiae
 C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
 C;Accession: S50608
 R;Dietrich, P.S.
 A;Description: The sequence of *S. cerevisiae* cosmids 9747, 8198, 9781, and lambda clones
 A;Reference number: S50436

RESULT 15

S59096
 AMP deaminase (EC 3.5.4.6) 2 isoform L - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Accession: S59096
 C;Date: 15-Feb-1996 #text_change 01-Mar-1996 #text_revision 01-Mar-1996
 R;van den Berg, P.; Sabina, R.L.
 Biochem. J. 311, 401-410, 1995
 A;Title: Characterization of human AMP deaminase 2 (AMPD2). Gene expression reveals a
 A;Reference number: S59094; PMID:9610174;
 A;Accession: S59096
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-605 <VAN>
 A;Cross-references: EMBL:U16269; NID:9608496; PID:AA06511.1; PMID:8526648
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
 C;Genetics:
 C;Superfamily: AMP deaminase
 C;Keywords: alternative splicing; hydrolase

Query Match 8.7%: Score 78.5; DB 2; Length 605;
 Best Local Similarity 25.7%; Pred. No. 22;
 Matches 38; Conservative 28; Mismatches 63; Indels 19; Gaps 8;
 A:Accession: S50608
 A;Molecule type: DNA
 A;Cross-references: 1-1391 <DB>
 C;Species: *Yarrowia lipolytica*
 C;Date: 29-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
 C;Accession: S50608
 R;Dietrich, P.S.
 A;Description: The sequence of *S. cerevisiae* cosmids 9747, 8198, 9781, and lambda clones
 A;Reference number: S50436

Qy 17 ATSCLLLALLYQGGAAPIS--SHCRUDKSNFQOPYTNRTPMALKASL----- 65
 Db 129 ASAALFFAHTI-----APIKSYSACRI--ARMDNNEFTINPSASLLNSDLDLFSVSGTK 180

Qy 66 ADNTTDVPLIGEKU-----PHGVSMSERCYLMKQVNLNFTEVLPFQPSDF- 111
 Db 181 SLNMIEMERSLGQNLNALBPLMDEALELAQKSRETCALYEEAFTPYNELLFKEGSGIV 240

Qy 112 -----QPMQEVYPPFIA-----RISRLSTCHIEGDLHIIQRTWQK 149
 Db 241 LNRLLQDQFDRITKGISSALSERENY--RISRLSTCHIEGDLHIIQRTWQK 300

Qy 150 DT 151
 Db 301 KT 302

Search completed: June 30, 2004, 19:33:29
 Job time : 22 secs

RESULT 14

S50608
 Hypothetical protein YER105C - Yeast (Saccharomyces cerevisiae)
 C;Species: Saccharomyces cerevisiae
 C;Accession: S50608
 R;Dietrich, P.S.
 A;Description: The sequence of *S. cerevisiae* cosmids 9747, 8198, 9781, and lambda clones
 A;Reference number: S50436

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:15:53 ; Search time 43 Seconds
(without alignments)
1176.843 Million cell updates/sec

Title: US-10-050-552A-2

Perfect score: 903

Sequence: 1 MAALQKSVSSPFLNGTLATSC.....EIKAIIGEIDLILFMSLRLNACI 179

Scoring table: BLOSUM62

Gapext 0.5

Maximum DB seq length: 20000000000

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:*

2: /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:*

3: /cgn2_6/_ptodata/2/pubpaas/US06_PUBCOMB.pep:*

4: /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:*

5: /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:*

6: /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:*

7: /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:*

8: /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:*

9: /cgn2_6/_ptodata/2/pubpaas/US09A_PUBCOMB.pep:*

10: /cgn2_6/_ptodata/2/pubpaas/US09B_PUBCOMB.pep:*

11: /cgn2_6/_ptodata/2/pubpaas/US09C_PUBCOMB.pep:*

12: /cgn2_6/_ptodata/2/pubpaas/US09 NEW_PUB.pep:*

13: /cgn2_6/_ptodata/2/pubpaas/US10A_PUBCOMB.pep:*

14: /cgn2_6/_ptodata/2/pubpaas/US10B_PUBCOMB.pep:*

15: /cgn2_6/_ptodata/2/pubpaas/US10C_PUBCOMB.pep:*

16: /cgn2_6/_ptodata/2/pubpaas/US10 NEW_PUB.pep:*

17: /cgn2_6/_ptodata/2/pubpaas/US60_NEW_PUB.pep:*

18: /cgn2_6/_ptodata/2/pubpaas/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|------------------|--------------------|
| 1 | 903 | 100.0 | 179 | 13 | US-10-050-552A-2 | Sequence 2, Appli |
| 2 | 903 | 100.0 | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 3 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 15, Appli |
| 4 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 2, Appli |
| 5 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 18, Appli |
| 6 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 7 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 8 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 9 | 897 | 99.3 | 179 | 9 | US-09-875-574-2 | Sequence 244, APP |
| 10 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 11 | 897 | 99.3 | 179 | 12 | US-09-955-052D-8 | Sequence 18, APP |
| 12 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 154, APP |
| 13 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 154, APP |
| 14 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 154, APP |
| 15 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 154, APP |

SEQUENCE ALIGNMENTS

| Sequence | Length | Score | DB ID | Length | Score | DB ID | Length | Score | DB ID |
|---|--------|-------|------------------|--------|-------|------------------|--------|-------|------------------|
| 1 MAALQKSVSSPFLNGTLATSC.....EIKAIIGEIDLILFMSLRLNACI | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 2 /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 3 /cgn2_6/_ptodata/2/pubpaas/US06_PUBCOMB.pep:* | 179 | 15 | US-10-050-552A-2 | 179 | 15 | US-10-050-552A-2 | 179 | 15 | US-10-050-552A-2 |
| 4 /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 5 /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:* | 179 | 9 | US-09-955-052D-8 | 179 | 9 | US-09-955-052D-8 | 179 | 9 | US-09-955-052D-8 |
| 6 /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:* | 179 | 9 | US-09-955-052D-8 | 179 | 9 | US-09-955-052D-8 | 179 | 9 | US-09-955-052D-8 |
| 7 /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:* | 179 | 10 | US-09-955-052D-8 | 179 | 10 | US-09-955-052D-8 | 179 | 10 | US-09-955-052D-8 |
| 8 /cgn2_6/_ptodata/2/pubpaas/US09A_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 9 /cgn2_6/_ptodata/2/pubpaas/US09B_PUBCOMB.pep:* | 179 | 15 | US-10-050-552A-2 | 179 | 15 | US-10-050-552A-2 | 179 | 15 | US-10-050-552A-2 |
| 10 /cgn2_6/_ptodata/2/pubpaas/US09C_PUBCOMB.pep:* | 179 | 14 | US-10-050-552A-2 | 179 | 14 | US-10-050-552A-2 | 179 | 14 | US-10-050-552A-2 |
| 11 /cgn2_6/_ptodata/2/pubpaas/US09 NEW_PUB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 12 /cgn2_6/_ptodata/2/pubpaas/US10A_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 13 /cgn2_6/_ptodata/2/pubpaas/US10B_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 14 /cgn2_6/_ptodata/2/pubpaas/US10C_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 15 /cgn2_6/_ptodata/2/pubpaas/US10 NEW_PUB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 16 /cgn2_6/_ptodata/2/pubpaas/US60_NEW_PUB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 17 /cgn2_6/_ptodata/2/pubpaas/US60_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |
| 18 /cgn2_6/_ptodata/2/pubpaas/US60_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 | 179 | 12 | US-10-050-552A-2 |

RESULTS

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|------------------|--------------------|
| 1 | 903 | 100.0 | 179 | 13 | US-10-050-552A-2 | Sequence 2, Appli |
| 2 | 903 | 100.0 | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 3 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 15, Appli |
| 4 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 2, Appli |
| 5 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 18, Appli |
| 6 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 7 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 8 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 9 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 10 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 11 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 12 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 13 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 14 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 15 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |

ALIGNMENTS

| Sequence | Length | Score | DB ID | Description |
|---|--------|-------|------------------|--------------------|
| 1 MAALQKSVSSPFLNGTLATSC.....EIKAIIGEIDLILFMSLRLNACI | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 2 /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 3 /cgn2_6/_ptodata/2/pubpaas/US06_PUBCOMB.pep:* | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 4 /cgn2_6/_ptodata/2/pubpaas/US07_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 5 /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:* | 179 | 9 | US-09-955-052D-8 | Sequence 15, Appli |
| 6 /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:* | 179 | 9 | US-09-955-052D-8 | Sequence 2, Appli |
| 7 /cgn2_6/_ptodata/2/pubpaas/US08_PUBCOMB.pep:* | 179 | 10 | US-09-955-052D-8 | Sequence 18, Appli |
| 8 /cgn2_6/_ptodata/2/pubpaas/US09A_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 9 /cgn2_6/_ptodata/2/pubpaas/US09B_PUBCOMB.pep:* | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 10 /cgn2_6/_ptodata/2/pubpaas/US09C_PUBCOMB.pep:* | 179 | 14 | US-10-050-552A-2 | Sequence 2, Appli |
| 11 /cgn2_6/_ptodata/2/pubpaas/US09 NEW_PUB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 12 /cgn2_6/_ptodata/2/pubpaas/US10A_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 13 /cgn2_6/_ptodata/2/pubpaas/US10B_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 14 /cgn2_6/_ptodata/2/pubpaas/US10C_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 15 /cgn2_6/_ptodata/2/pubpaas/US10 NEW_PUB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 16 /cgn2_6/_ptodata/2/pubpaas/US60_NEW_PUB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 17 /cgn2_6/_ptodata/2/pubpaas/US60_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |
| 18 /cgn2_6/_ptodata/2/pubpaas/US60_PUBCOMB.pep:* | 179 | 12 | US-10-050-552A-2 | Sequence 2, Appli |

RESULTS

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|------------------|--------------------|
| 1 | 903 | 100.0 | 179 | 13 | US-10-050-552A-2 | Sequence 2, Appli |
| 2 | 903 | 100.0 | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 3 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 15, Appli |
| 4 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 2, Appli |
| 5 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 18, Appli |
| 6 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 7 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 8 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 9 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 10 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 11 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 12 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 13 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 14 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 15 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |

RESULTS

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|------------------|--------------------|
| 1 | 903 | 100.0 | 179 | 13 | US-10-050-552A-2 | Sequence 2, Appli |
| 2 | 903 | 100.0 | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 3 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 15, Appli |
| 4 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 2, Appli |
| 5 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 18, Appli |
| 6 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 7 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 8 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 9 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 10 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 11 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 12 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 13 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 14 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 15 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |

RESULTS

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|------------------|--------------------|
| 1 | 903 | 100.0 | 179 | 13 | US-10-050-552A-2 | Sequence 2, Appli |
| 2 | 903 | 100.0 | 179 | 15 | US-10-050-552A-2 | Sequence 2, Appli |
| 3 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 15, Appli |
| 4 | 897 | 99.3 | 179 | 9 | US-09-955-052D-8 | Sequence 2, Appli |
| 5 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 18, Appli |
| 6 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 7 | 897 | 99.3 | 179 | 10 | US-09-955-052D-8 | Sequence 2, Appli |
| 8 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 9 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 10 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 11 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 12 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 13 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 14 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |
| 15 | 897 | 99.3 | 179 | 12 | US-10-050-552A-2 | Sequence 244, APP |

RESULTS

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|-------|-------------|
| 1 | 903 | | | | | |

Qy 121 FIARISNLSTCHIEGDDLHQVNRQKLKDVTVKIGESEBIRAKIGELDILFMSLRNACI 179
 Db 121 FIARISNLSTCHIEGDDLHQVNRQKLKDVTVKIGESEBIRAKIGELDILFMSLRNACI 179

RESULT 2
 US-10-238-965-2
 i Sequence 2, Application US/10238965
 i Publication No. US200400002586A1
 i GENERAL INFORMATION:
 i APPLICANT: Nagen, Ronald A.P.
 i APPLICANT: Colau, Didier
 i APPLICANT: Renaud, Jean-Christophe
 i APPLICANT: Dumont, Laure
 i APPLICANT: Polikarpov, Igor
 i TITLE OF INVENTION: Crystal structure of Interleukin-22
 i FILE REFERENCE: LUD-5722 US
 i CURRENT APPLICATION NUMBER: US10/238,965
 i CURRENT FILING DATE: 2002-09-10
 i PRIOR APPLICATION NUMBER: 60/317,937
 i PRIOR FILING DATE: 2001-09-10
 i PRIOR APPLICATION NUMBER: 60/333,150
 i PRIOR FILING DATE: 2001-11-27
 i NUMBER OF SEQ ID NOS: 5
 i SOFTWARE: PatentIn version 3.1
 i SEQ ID NO: 2
 i LENGTH: 179
 i TYPE: PRT
 i ORGANISM: Homo sapiens

US-10-238-965-2

Query Match 100.0%; Score 903; DB 15; Length 179;
 Best Local Similarity 100.0%; Pred. No. 9e-92; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 179; Conservative 0; Mi matches 0; Indels 0; Gaps 0;

-

Qy 1 MAALQKSVSSFLMGTATSCLLALIYOGGAAAPISSHCRDLKSNFOQPYITNRTFMLA 60
 Db 1 MAALQKSVSSFLMGTATSCLLALIYOGGAAAPISSHCRDLKSNFOQPYITNRTFMLA 60

Qy 61 KEASLADNTDVLIGEFLPHGYSMSERCYLMKQVNLNFTLBEVLFPQSDRFQPYQEVYP 120
 Db 61 KEASLADNTDVLIGEFLPHGYSMSERCYLMKQVNLNFTLBEVLFPQSDRFQPYQEVYP 120

Qy 121 FIARISNLSTCHIEGDDLHQVNRQKLKDVTVKIGESEBIRAKIGELDILFMSLRNACI 179
 Db 121 FIARISNLSTCHIEGDDLHQVNRQKLKDVTVKIGESEBIRAKIGELDILFMSLRNACI 179

RESULT 3
 JS-09-728-911-15
 i Sequence 15, Application US/09728911
 i GENERAL INFORMATION:
 i APPLICANT: Presnall, Scott R.
 i APPLICANT: Xu, Wenfeng
 i APPLICANT: Kindsvogel, Wayne
 i APPLICANT: Chen, Zhi
 i TITLE OF INVENTION: Human Cytokine Receptor
 i FILE REFERENCE: 99-93
 i CURRENT APPLICATION NUMBER: US/09/728,911
 i CURRENT FILING DATE: 2000-12-01
 i PRIOR APPLICATION NUMBER: US 60/169,043
 i PRIOR FILING DATE: 1999-12-03
 i PRIOR APPLICATION NUMBER: US 60/232,219
 i PRIOR FILING DATE: 2000-09-13
 i NUMBER OF SEQ ID NOS: 36
 i SOFTWARE: FastSEQ for Windows Version 3.0
 i SEQ ID NO: 15
 i LENGTH: 179
 i TYPE: PRT
 i ORGANISM: Homo sapiens

RESULT 4
 US-09-870-574-2
 i Sequence 2, Application US/09870574
 i Patent No. US20020102723A1
 i GENERAL INFORMATION:
 i APPLICANT: Gurley, Austin L.
 i APPLICANT: Aggarwal, Sudipta
 i APPLICANT: Xie, Ming-Hong
 i APPLICANT: Maruoka, Brien M.
 i APPLICANT: Foster, Jessica S.
 i APPLICANT: Goddard, Audrey
 i APPLICANT: Wood, William T.
 i TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
 i TITLE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDER
 i FILE REFERENCE: P2806-1 (US)
 i CURRENT APPLICATION NUMBER: US/09/870,574
 i CURRENT FILING DATE: 2001-05-30
 i PRIOR APPLICATION NUMBER: US 60/169,495
 i PRIOR FILING DATE: 1999-12-07
 i PRIOR APPLICATION NUMBER: PCT/US00/14042
 i PRIOR FILING DATE: 2000-05-22
 i PRIOR APPLICATION NUMBER: PCT/US00/233328
 i PRIOR FILING DATE: 2000-08-24
 i NUMBER OF SEQ ID NOS: 7
 i SEQ ID NO: 2
 i LENGTH: 179
 i TYPE: PRT
 i ORGANISM: Homo Sapien

US-09-870-574-2

Query Match 99.3%; Score 897; DB 9; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 176; Conservative 3; Mi matches 0; Indels 0; Gaps 0;

-

Qy 1 MAALQKSVSSFLMGTATSCLLALIYOGGAAAPISSHCRDLKSNFOQPYITNRTFMLA 60
 Db 1 MAALQKSVSSFLMGTATSCLLALIYOGGAAAPISSHCRDLKSNFOQPYITNRTFMLA 60

Qy 61 KEASLADNTDVLIGEFLPHGYSMSERCYLMKQVNLNFTLBEVLFPQSDRFQPYQEVYP 120
 Db 61 KEASLADNTDVLIGEFLPHGYSMSERCYLMKQVNLNFTLBEVLFPQSDRFQPYQEVYP 120

Qy 121 FIARISNLSTCHIEGDDLHQVNRQKLKDVTVKIGESEBIRAKIGELDILFMSLRNACI 179
 Db 121 FIARISNLSTCHIEGDDLHQVNRQKLKDVTVKIGESEBIRAKIGELDILFMSLRNACI 179

RESULT 5
 US-09-565-528-18
 i Sequence 18, Application US/09965528
 i Publication No. US20020187523A1
 i GENERAL INFORMATION:
 i APPLICANT: INCYTE GENOMICS, INC.
 i APPLICANT: TANG, Y. Tom

APPLICANT: YUE, Henry
 APPLICANT: LAL, Preeti
 APPLICANT: BURFORD, Neil
 APPLICANT: BANDMAN, Olga
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: AZIMZAI, Yalda
 APPLICANT: LU, Duyng Aina M.
 APPLICANT: PATTERSON, Chandra
 TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
 FILE REFERENCE: PE-0701 USA
 CURRENT APPLICATION NUMBER: US/09/965,528
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/134,949
 PRIOR FILING DATE: 1999-05-19
 PRIOR APPLICATION NUMBER: 60/144,220
 PRIOR FILING DATE: 1999-07-15
 PRIOR APPLICATION NUMBER: 60/146,700
 PRIOR FILING DATE: 1999-07-10
 PRIOR APPLICATION NUMBER: 60/157,508
 PRIOR FILING DATE: 1999-10-04
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: PERL Program
 SEQ ID NO: 18
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20020187523A1 5571181CD1
 US-09-965-528-18

Query Match: 1 MAALQKSVSSPLMGLATSCULLALLVCGAAAPISSHCRDLDSNFOQQYITNRTFMLA 60
 Matches 176; Conservative 98.3%; Score 897; DB 9; Length 179;
 Pred. No. 4 2e-31; 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSPLMGLATSCULLALLVCGAAAPISSHCRDLDSNFOQQYITNRTFMLA 60
 Db 1 MAALQKSVSSPLMGLATSCULLALLVCGAAAPISSHCRDLDSNFOQQYITNRTFMLA 60

Qy 61 KEASLADNNTDVRLIGEKLPHGVMSERCYLMKQVINTLLEVLFPQSDRFQPMQEYVP 120
 Db 61 KEASLADNNTDVRLIGEKLPHGVMSERCYLMKQVINTLLEVLFPQSDRFQPMQEYVP 120

Qy 121 FLARLSNRSLSTCHIEGDDLHQIQRVYKLTKVKGSGEIKAGBDLLFMSLRNACI 179
 Db 121 FLARLSNRSLSTCHIEGDDLHQIQRVYKLTKVKGSGEIKAGBDLLFMSLRNACI 179

RESULT 6
 US-09-925-055D-8
 Sequence B, Application US/09/925055D
 GENERAL INFORMATION:
 APPLICANT: Kindsvogel, Wayne R.
 APPLICANT: Topouzis, Stavros
 TITLE OF INVENTION: SOLUBLE CYTOKINE RECEPTORS
 FILE REFERENCE: 00-56
 CURRENT APPLICATION NUMBER: US/09/925,055D
 CURRENT FILING DATE: 2003-08-08
 PRIOR APPLICATION NUMBER: US 60/223,827
 PRIOR FILING DATE: 2000-08-08
 PRIOR APPLICATION NUMBER: US 60/250,876
 PRIOR FILING DATE: 2000-12-01
 SOFTWARE: Fast-SEQ for Windows Version 3.0
 SEQ ID NO: 8
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-925-055D-8

Query Match: 1 MAALQKSVSSPLMGLATSCULLALLVCGAAAPISSHCRDLDSNFOQQYITNRTFMLA 60
 Matches 176; Conservative 98.3%; Score 897; DB 10; Length 179;
 Pred. No. 4 2e-91; 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSPLMGLATSCULLALLVCGAAAPISSHCRDLDSNFOQQYITNRTFMLA 60
 Db 1 MAALQKSVSSPLMGLATSCULLALLVCGAAAPISSHCRDLDSNFOQQYITNRTFMLA 60

Qy 61 KEASLADNNTDVRLIGEKLPHGVMSERCYLMKQVINTLLEVLFPQSDRFQPMQEYVP 120
 Db 61 KEASLADNNTDVRLIGEKLPHGVMSERCYLMKQVINTLLEVLFPQSDRFQPMQEYVP 120

Qy 121 FLARLSNRSLSTCHIEGDDLHQIQRVYKLTKVKGSGEIKAGBDLLFMSLRNACI 179
 Db 121 FLARLSNRSLSTCHIEGDDLHQIQRVYKLTKVKGSGEIKAGBDLLFMSLRNACI 179

RESULT 8
 US-10-081-056-354
 Sequence 35, Application US/10081056
 Publication No. US2004004327A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Gerber, Hans Peter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Masters, Scott A.
 APPLICANT: Pan, James
 APPLICANT: Paon, Nicholas F.
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Ye, Weilian
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSTICS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 FILE REFERENCE: P2235P1C1
 CURRENT APPLICATION NUMBER: US/10/081,056
 CURRENT FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: PCT/US01/21735
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US/60/219,556
 PRIOR FILING DATE: 2000-07-20
 PRIOR APPLICATION NUMBER: US/60/220,624
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US/60/220,664
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US/60/222,695
 PRIOR FILING DATE: 2000-08-02
 PRIOR APPLICATION NUMBER: US/60/230,977
 PRIOR FILING DATE: 2000-08-17
 PRIOR APPLICATION NUMBER: PCT/US00/23522
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: PCT/US00/23328
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US/60/230,978
 PRIOR FILING DATE: 2000-09-07
 PRIOR APPLICATION NUMBER: US/60/000,000
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US/60/664,610
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: US/60/665,350
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: US/60/242,922
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US/60/242,938
 PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: PCT/US03/30873
 PRIOR FILING DATE: 2000-11-10
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: 2000-12-01
 PRIOR APPLICATION NUMBER: US/60/2359
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: PCT/US03/34956
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: US/60/767,609
 PRIOR FILING DATE: 2001-01-22
 PRIOR APPLICATION NUMBER: US/60/796,498
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: PCT/US01/06530
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: PCT/US01/06556
 PRIOR FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: US/60/802,785
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: US/60/808,639
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: US/60/816,744
 PRIOR FILING DATE: 2001-03-22
 PRIOR APPLICATION NUMBER: US/60/828,356
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: US/60/854,238
 PRIOR FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: US/60/854,280
 PRIOR FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: US/60/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US/60/866,034
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: PCT/US01/17092

PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: US/09/870,574
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: PCT/US01/17443
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: PCT/US01/17800
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: PCT/US01/19692
 PRIOR FILING DATE: 2001-06-20
 PRIOR APPLICATION NUMBER: PCT/US01/00000
 PRIOR FILING DATE: 2001-06-28
 NUMBER OF SEQ ID NOS: 383
 SEQ ID NO: 354
 LENGTH: 179
 TYPE: PRT
 ORGANISM: *Homosapiens*
 US-10-081-056-354

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTIATSCILLALLVQGAAAPISSHCRDLSKNSFQQPYITNTFMLA 60
 Db 1 MAALQKSVSSFLMGTIATSCILLALLVQGAAAPISSHCRDLSKNSFQQPYITNTFMLA 60

Qy 61 KEASLADNTDVRLIGEKLFGVMSERCYLMKQVNLNFTEEVLPQSDRFQPMQEYVVP 120
 Db 61 KEASLADNTDVRLIGEKLFGVMSERCYLMKQVNLNFTEEVLPQSDRFQPMQEYVVP 120

Qy 121 FIAIRSNRLSTCHEGDDLHTQRYQKLKDTVKIGEBSGRKIAIGBDLIFMSLRNACI 179
 Db 121 FIAIRSNRLSTCHEGDDLHTQRYQKLKDTVKIGEBSGRKIAIGBDLIFMSLRNACI 179

RESULT 9
 US-10-219-535-244
 Sequence 244, Application US/10219535
 Publication No. US200400417941
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Dennoyers, Luc
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanaabe, Colin L.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3530P1C60
 CURRENT APPLICATION NUMBER: US/10/219,535
 CURRENT FILING DATE: 2002-08-14
 PRIOR APPLICATION NUMBER: 10/119,480
 PRIOR FILING DATE: 2002-04-09
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063549
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/064103
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/069873
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079566

PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079728
 Remaining Prior Application data removed - See File Wrapper or PALM.

SEQ ID NO 244 LENGTH: 179 TYPE: PRT ORGANISM: Homo Sapien US-10-219-535-244

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGLATSCLLALIVQGAAPISCHCRDJSNFOQPYITNRITFMLA 60
 Db 1 MAALQKSVSSFLMGLATSCLLALIVQGAAPISCHCRDJSNFOQPYITNRITFMLA 60
 Qy 61 KEASLADNTDVLIGKELFQMSMRSERCYLMKQVNLFTLEFLVLFQSDRFQPYMQEVYP 120
 Db 1 MAALQKSVSSFLMGLATSCLLALIVQGAAPISCHCRDJSNFOQPYITNRITFMLA 60
 Qy 61 KEASLADNTDVLIGKELFQMSMRSERCYLMKQVNLFTLEFLVLFQSDRFQPYMQEVYP 120
 Db 61 KEASLADNTDVLIGKELFQMSMRSERCYLMKQVNLFTLEFLVLFQSDRFQPYMQEVYP 120

RESULT 11
 US-09-969-984-18
 Sequence 18, Application US/09969984
 Publication No. US2004004824A1
 GENERAL INFORMATION:
 APPLICANT: INCYTE GENOMICS, INC.
 APPLICANT: TANG, Y. Tom
 APPLICANT: YUE, Henry
 APPLICANT: LAL, Preeti
 APPLICANT: BURFORD, Neil
 APPLICANT: BANDMAN, Olga
 APPLICANT: BAUGRIN, Mariah R.
 APPLICANT: AZIMZAI, Yalda
 APPLICANT: LU, Dyung Aina M.
 APPLICANT: PATTERSON, Chandra
 TITLE OF INVENTION: EXTRACHLORAL SIGNALING MOLECULES
 FILE REFERENCE: PF-0701-1 USA
 CURRENT APPLICATION NUMBER: US/09/969,984
 CURRENT FILING DATE: 2001-10-02
 PRIOR APPLICATION NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508
 PRIOR FILING DATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: PERL Program
 SEQ ID NO 18
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20040048244A1 5571181CD1
 US-09-969-984-18

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGLATSCLLALIVQGAAPISCHCRDJSNFOQPYITNRITFMLA 60
 Db 1 MAALQKSVSSFLMGLATSCLLALIVQGAAPISCHCRDJSNFOQPYITNRITFMLA 60
 Qy 61 KEASLADNTDVLIGKELFQMSMRSERCYLMKQVNLFTLEFLVLFQSDRFQPYMQEVYP 120
 Db 61 KEASLADNTDVLIGKELFQMSMRSERCYLMKQVNLFTLEFLVLFQSDRFQPYMQEVYP 120
 Qy 121 FIARISNRSLSTCHIEGDDLHIONVQKLDTVKIGESGRKAIGEGLDLMFLMSLRNACI 179
 Db 121 FIARISNRSLSTCHIEGDDLHIONVQKLDTVKIGESGRKAIGEGLDLMFLMSLRNACI 179
 REMAINING Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 246
 SEQ ID NO 244 LENGTH: 179

RESULT 12
 US-10-063-745-154
 Sequence 154, Application US/10063745

Publication No. US20040058411A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,745
 CURRENT FILING DATE: 2002-05-09
 Prior Application Removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 179
 SEQ ID NO 154
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-063-745-154

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 Db 61 KEASLADNNTDVRLIGEKLPHGVSMSERCYLMQKVINFTEEVLFQSDRFQPYMEQVVP 120
 61 KEASLADNNTDVRLIGEKLPHGVSMSERCYLMQKVINFTEEVLFQSDRFQPYMEQVVP 120
 Qy 121 FLARLSNRLSTCHIEGDDLHQIQRNVQKLKDVKLGESEKIAIGELLLFMSLRNACT 179
 Db 121 FLARLSNRLSTCHIEGDDLHQIQRNVQKLKDVKLGESEKIAIGELLLFMSLRNACT 179

RESULT 13
 US-10-063-512-154
 Sequence 154, Application US/10063512
 Publication No. US20030018183A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,512
 CURRENT FILING DATE: 2002-05-01
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 154
 LENGTH: 179
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-063-512-154

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 Db 61 KEASLADNNTDVRLIGEKLPHGVSMSERCYLMQKVINFTEEVLFQSDRFQPYMEQVVP 120
 61 KEASLADNNTDVRLIGEKLPHGVSMSERCYLMQKVINFTEEVLFQSDRFQPYMEQVVP 120
 Qy 121 FLARLSNRLSTCHIEGDDLHQIQRNVQKLKDVKLGESEKIAIGELLLFMSLRNACT 179
 Db 121 FLARLSNRLSTCHIEGDDLHQIQRNVQKLKDVKLGESEKIAIGELLLFMSLRNACT 179

RESULT 14
 US-10-063-513-154
 Sequence 154, Application US/10063513
 Publication No. US20030018172A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 Db 61 KEASLADNNTDVRLIGEKLPHGVSMSERCYLMQKVINFTEEVLFQSDRFQPYMEQVVP 120
 61 KEASLADNNTDVRLIGEKLPHGVSMSERCYLMQKVINFTEEVLFQSDRFQPYMEQVVP 120
 Qy 121 FLARLSNRLSTCHIEGDDLHQIQRNVQKLKDVKLGESEKIAIGELLLFMSLRNACT 179
 Db 121 FLARLSNRLSTCHIEGDDLHQIQRNVQKLKDVKLGESEKIAIGELLLFMSLRNACT 179

RESULT 15
 US-10-063-515-154
 Sequence 154, Application US/10063515
 Publication No. US20030018173A1
 GENERAL INFORMATION:
 APPLICANT: Eaton, Dan L.
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3230R1C1

Query Match 99.3%; Score 897; DB 12; Length 179;
 Best Local Similarity 98.3%; Pred. No. 4.2e-91;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60
 1 MAALQKSVSSFLMGTATSCLLALIVQGAAPISSHCRDKSNFQDQPYITNRTEMLA 60

CURRENT APPLICATION NUMBER: US/10/063,515
PRIORITY FILING DATE: 2002-01-01
PRIORITY APPLICATION REMOVED - SEE FILE WRAPPER OR PAM
NUMBER OF SEQ ID NOS: 170
SEQ ID NO: 154
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapien
US-10-063-515-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91; Length 179;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSETLMGITLATSCLLALLIYQGGAAAPISSHCRDLDKSNFOQPTTNTRPFMLA 60
Db 1 MAALQKSVSETLMGITLATSCLLALLIYQGGAAAPISSHCRDLDKSNFOQPTTNTRPFMLA 60
QY 61 KEASLADNTNDVRLIGKLFHGVMSMSRCLMKQVINFITLEVLFPQDFQPYMQEVVP 120
Db 61 KEASLADNTNDVRLIGKLFHGVMSMSRCLMKQVINFITLEVLFPQDFQPYMQEVVP 120
QY 121 FLARLSNRLSTCHIEGDDLHQRNVQKLDTVKGESGEIKAIAGELDLFMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDLHQRNVQKLDTVKGESGEIKAIAGELDLFMSLRNACI 179

Search completed: June 30, 2004, 19:29:39
Job time : 44 secs

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1 | 897 | 99.3 | 179 | 3 | AAV22879 | Aay92879 Human T c |
| 2 | 897 | 99.3 | 179 | 3 | AAB36292 | Aab36292 Human GIL |
| 3 | 897 | 99.3 | 179 | 4 | AAB31210 | Aab31210 Amino aci |
| 4 | 897 | 99.3 | 179 | 4 | AAB04538 | Aae04538 Human cyt |
| 5 | 897 | 99.3 | 179 | 4 | AAB87602 | Aab87602 Human PRO |
| 6 | 897 | 99.3 | 179 | 4 | AAB62664 | Aab62664 Human IL- |
| 7 | 897 | 99.3 | 179 | 4 | AAB48074 | Aab48074 Human ext |
| 8 | 897 | 99.3 | 179 | 5 | AAB93713 | Aab93713 Human PRO |
| 9 | 897 | 99.3 | 179 | 5 | AAE19237 | Aae19237 Human TIF |
| 10 | 897 | 99.3 | 179 | 5 | ABG5927 | Abg95927 Human sec |
| 11 | 897 | 99.3 | 179 | 5 | ABD44993 | Abd44993 Human PRO |
| 12 | 897 | 99.3 | 179 | 5 | AAT78081 | Aau78081 Human inc |
| 13 | 897 | 99.3 | 179 | 5 | AAB28608 | Aae28608 Human int |
| 14 | 897 | 99.3 | 179 | 5 | AAT76909 | Aau76909 Human int |
| 15 | 897 | 99.3 | 179 | 5 | ABB95599 | Abb95599 Human arg |
| 16 | 897 | 99.3 | 179 | 5 | ABE79910 | Abb79910 Human int |
| 17 | 897 | 99.3 | 179 | 6 | ABU90860 | Abu90860 Human PRO |
| 18 | 897 | 99.3 | 179 | 6 | ABO25181 | Abo25181 Novel hum |
| 19 | 897 | 99.3 | 179 | 6 | ABO33826 | Abo33826 Novel hum |
| 20 | 897 | 99.3 | 179 | 6 | ABU90952 | Abu90952 Novel hum |
| 21 | 897 | 99.3 | 179 | 6 | ABD34011 | Abo34011 Human sec |
| 22 | 897 | 99.3 | 179 | 6 | ABU72028 | Abu72028 Novel hum |
| 23 | 897 | 99.3 | 179 | 6 | ABD67299 | Abd67299 Novel hum |
| 24 | 897 | 99.3 | 179 | 6 | ABU71582 | Abu71582 Novel hum |
| 25 | 897 | 99.3 | 179 | 6 | ABU72363 | Abu72363 Human PRO |

ALIGNMENTS

RESULT 1
ID: AAY92879 standard; protein; 179 AA.
XX
AC: AAY92879;
XX
DT: 04-SEP-2000 (first entry)
XX
DE: Human T cell inducible factor.
XX
KW: TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW: Anti-allergic; cytostatic; inhibitor; antagonist; chromosome 12q15.
XX
OS: Homo sapiens.
XX
PN: WO200024758-A1.
XX
PD: 04-MAY-2000.
XX
PP: 18-OCT-1999;
XX
PR: 26-OCT-1998;
PR: 16-JUL-1999;
XX
RU(DW) LUDWIG INST CANCER RES.
XX
PI: Dumoutier L, Louhed J, Renaud J,
XX
DR: WPI; 2000-422495/36.
DR: N-PSDB; AAA28839, AAA28840.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| # | Query | Match | Length | DB | ID | Description |
|----|-------|-------|--------|----|----------|--------------------|
| 1 | 897 | 99.3 | 179 | 3 | AAV22879 | Aay92879 Human T c |
| 2 | 897 | 99.3 | 179 | 3 | AAB36292 | Aab36292 Human GIL |
| 3 | 897 | 99.3 | 179 | 4 | AAB31210 | Aab31210 Amino aci |
| 4 | 897 | 99.3 | 179 | 4 | AAB04538 | Aae04538 Human cyt |
| 5 | 897 | 99.3 | 179 | 4 | AAB87602 | Aab87602 Human PRO |
| 6 | 897 | 99.3 | 179 | 4 | AAB62664 | Aab62664 Human IL- |
| 7 | 897 | 99.3 | 179 | 4 | AAB48074 | Aab48074 Human ext |
| 8 | 897 | 99.3 | 179 | 5 | AAB93713 | Aab93713 Human PRO |
| 9 | 897 | 99.3 | 179 | 5 | AAE19237 | Aae19237 Human TIF |
| 10 | 897 | 99.3 | 179 | 5 | ABG5927 | Abg95927 Human sec |
| 11 | 897 | 99.3 | 179 | 5 | ABD44993 | Abd44993 Human PRO |
| 12 | 897 | 99.3 | 179 | 5 | AAT78081 | Aau78081 Human inc |
| 13 | 897 | 99.3 | 179 | 5 | AAB28608 | Aae28608 Human int |
| 14 | 897 | 99.3 | 179 | 5 | AAT76909 | Aau76909 Human int |
| 15 | 897 | 99.3 | 179 | 5 | ABB95599 | Abb95599 Human arg |
| 16 | 897 | 99.3 | 179 | 5 | ABE79910 | Abb79910 Human int |
| 17 | 897 | 99.3 | 179 | 6 | ABU90860 | Abu90860 Human PRO |
| 18 | 897 | 99.3 | 179 | 6 | ABO25181 | Abo25181 Novel hum |
| 19 | 897 | 99.3 | 179 | 6 | ABO33826 | Abo33826 Novel hum |
| 20 | 897 | 99.3 | 179 | 6 | ABU90952 | Abu90952 Novel hum |
| 21 | 897 | 99.3 | 179 | 6 | ABD34011 | Abo34011 Human sec |
| 22 | 897 | 99.3 | 179 | 6 | ABU72028 | Abu72028 Novel hum |
| 23 | 897 | 99.3 | 179 | 6 | ABD67299 | Abd67299 Novel hum |
| 24 | 897 | 99.3 | 179 | 6 | ABU71582 | Abu71582 Novel hum |
| 25 | 897 | 99.3 | 179 | 6 | ABU72363 | Abu72363 Human PRO |

This is the human T cell derived inducible factor (TIF). The gene was mapped to chromosome 12q15. The human TIF was identified based on homology to a murine TIF, which was identified by subtraction cloning from a murine lymphoma cell line BW5147 in the presence or absence of IL-9. BW5147, can be grown in vitro, without the need to add any cytokines to its culture medium. Many IL-9 activities are mediated by activation of STAT transcription factors. The novel TIFs were expressed in the presence of IL-9, but not in its absence. TIFs induce STAT activation in cells. They can be used, e.g. in the stimulation of regeneration of targeted tissues. Their inhibitors or antagonists can be used to retard, prevent or inhibit differentiation of other tissues. The

TIFs and their coding sequences are useful in the treatment of asthma, allergies and lymphoma (claimed). They are also useful for identifying compounds that inhibit or activate T cell induced factor activity in a cell (claimed).

TIFs and their coding sequences are useful in the treatment of asthma, allergies and lymphoma (claimed). They are also useful for identifying compounds that inhibit or activate T cell induced factor activity in a cell (claimed).

PR 20-MAR-2000; 2000W0-US007377.
 PR 30-MAR-2000; 2000W0-US008439.
 PR 15-MAY-2000; 2000W0-US013356.
 PR 17-MAY-2000; 2000W0-US013705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PT Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers I, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen MG, Goddard A;
 PI Godowski PU, Gunney AB, Kijaviv JH, Mather JP, Napier MA, Par J;
 PI Paoni NF, Roy MA, Stewart TA, Tummas D, Wattanabe CK, Williams EM;
 PI Wood WI, Zhang Z;
 XX
 DR; 20001-050091/06.
 XX
 DR N-PSDB; AACB7053.
 XX
 CC The present sequence represents a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO212, PRO288, PRO248, PRO1361, PRO1308, PRO1272, PRO1419, PRO999, PRO170, PRO337, PRO1411, PRO4356, PRO246, PRO255, PRO941, PRO1096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene
 XX
 Sequence 179 AA;

Query Match 99.3%; Score 897; DB 4; Length 179;
 Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSPMLGTLATSCILLALIIVQGAAAPISSCPDKSNFQOQYITNRTPEMLA 60
 Db 1 MAALQKSVSSPMLGTLATSCILLALIIVQGAAAPISSCPDKSNFQOQYITNRTPEMLA 60
 QY 61 KEASLADNTNDVRLIGKLEKQHGVMSERCYLMQVNLFTLKEVLFFQSDRFOFYMOEVVP 120
 Db 61 KEASLADNTNDVRLIGKLEKQHGVMSERCYLMQVNLFTLKEVLFFQSDRFOFYMOEVVP 120
 QY 121 FLARLSNRLSTKCHIEGDDLHQTRVQLKQDVKVKGSEGEIKAGELDDEMSLRNACI 179
 Db 121 FLARLSNRLSTKCHIEGDDLHQTRVQLKQDVKVKGSEGEIKAGELDDEMSLRNACI 179

RESULT 4
 AAE04538
 XX AAE04538 standard; protein; 179 AA.
 AC AAE04538;
 XX DT 10-SEP-2001 (first entry)
 DE Human cytokine, ZCYT018 protein #1.
 KW Human; cytosolic; cytokine; ZCYT018 protein; genetic abnormality;
 KW cancer; inflammation; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200116318-A2.

PR 20-MAR-2000; 2000W0-US007377.
 PR 30-MAR-2000; 2000W0-US008439.
 PR 15-MAY-2000; 2000W0-US013356.
 PR 17-MAY-2000; 2000W0-US013705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PT Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers I, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen MG, Goddard A;
 PI Godowski PU, Gunney AB, Kijaviv JH, Mather JP, Napier MA, Par J;
 PI Paoni NF, Roy MA, Stewart TA, Tummas D, Wattanabe CK, Williams EM;
 PI Wood WI, Zhang Z;
 XX
 DR; 20001-050091/06.
 XX
 DR N-PSDB; AACB7053.
 XX
 CC The present sequence represents a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO212, PRO288, PRO248, PRO1361, PRO1308, PRO1272, PRO1419, PRO999, PRO170, PRO337, PRO1411, PRO4356, PRO246, PRO255, PRO941, PRO1096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene
 XX
 Sequence 179 AA;

Query Match 99.3%; Score 897; DB 4; Length 179;
 Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSPMLGTLATSCILLALIIVQGAAAPISSCPDKSNFQOQYITNRTPEMLA 60
 Db 1 MAALQKSVSSPMLGTLATSCILLALIIVQGAAAPISSCPDKSNFQOQYITNRTPEMLA 60
 QY 61 KEASLADNTNDVRLIGKLEKQHGVMSERCYLMQVNLFTLKEVLFFQSDRFOFYMOEVVP 120
 Db 61 KEASLADNTNDVRLIGKLEKQHGVMSERCYLMQVNLFTLKEVLFFQSDRFOFYMOEVVP 120
 QY 121 FLARLSNRLSTKCHIEGDDLHQTRVQLKQDVKVKGSEGEIKAGELDDEMSLRNACI 179
 Db 121 FLARLSNRLSTKCHIEGDDLHQTRVQLKQDVKVKGSEGEIKAGELDDEMSLRNACI 179

RESULT 5
 AAB87602
 ID AAB87602 standard; protein; 179 AA.
 XX
 AC AAB87602;
 XX DT 15-MAY-2001 (first entry)
 DE Human PRO10096.
 KW Human; PRO protein; mapping.
 XX OS Homo sapiens.
 XX PN WO200116318-A2.

2010-03-03 14:26:44 PAB62664 standard; protein; 179 AA.
XX

AB48074 standard; protein; 179 AA.
ID AB48074
YY

AA AC
AB48074;
XX

DE Human IL-TIF polypeptide.
 DE Human IL-TIF receptor; zcytoster; IL-TIF; antiinflammatory; cytostatic;
 DE Human extracellular signaling molecule (ECOS) (ID 5521181CDN)
 DT 19-MAR-2001 (first entry)
 XX

| | | | |
|----|--|--|---|
| XX | Extracellular signaling molecule; EXCS; anti-inflammatory; human; immunosuppressive; cytotoxic; neuroprotective; gastrointestinal; virucide; antibacterial; anti-HIV; human immunodeficiency virus; antinefertile; cerebroprotective; nootropic; antiulcer; antifungal; anticonvulsant; tranquilizer; neuroleptic; vasotropics; gynecological; keratolytic; protozoacide; gene therapy. | Db | 1 MAALQKSVSSFLMGTATLSCILLALLVQGGAAPISSHCRLDKSNFQQPYITINRPFMLA 60 |
| XX | Homo sapiens. | Qy | 61 KRSASLDNNITVRLIGEKLFQGVNSNSRCYLMQKVINFTRLEVLLFPOSDFRQPYMDEVP 120 |
| XX | W0200070049-A2. | Db | 61 KRSASLDNNITVRLIGEKLFQGVNSNSRCYLMQKVINFTRLEVLLFPOSDFRQPYMDEVP 120 |
| XX | 23-NOV-2000. | Qy | 121 FIAARTSNRLSTCHIISDDFLHQRNYVQKLKOTVVKLGESEGETKAGBLDLFMSLRVACI 179 |
| XX | PD | Db | 121 FLARLSNRLSTCHIISDDFLHQRNYVQKLKOTVVKLGESEGETKAGBLDLFMSLRVACI 179 |
| XX | 23-NOV-2000; 2000W0-US013975. | RESULT 8 | XX |
| XX | 19-MAY-1999; 99US-0134949P. | AAU83713 standard; protein; 179 AA. | XX |
| PR | 19-MAY-1999; 99US-0144270P. | ID AAU83713 | AC AAU83713; |
| PR | 30-JUL-1999; 99US-0146700P. | XX | DT 08-MAY-2002 (first entry) |
| PR | 04-OCT-1999; 99US-0157508P. | XX | DE Human PRO protein, Seq ID NO 244. |
| XX | PA (INCYT -) INCYTE GENOMICS INC. | XX | XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha. |
| XX | PT Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR; PT Azimzai Y, Lu DAM, Patterson C; DR 2001-025021/03. | XX | XX Homo Sapiens. |
| XX | PT New human extracellular signaling nucleic acids and polypeptides useful for diagnosing, treating and preventing infections and gastrointestinal, neurological, reproductive, and autoimmune/inflammatory disorders. | XX | XX WO200209288-A2. |
| XX | PS Claim 1; Page 94; 114pp; English. | PD 31-JAN-2002. | XX |
| XX | CC The invention provides human extracellular signaling molecules (EXCS) and polynucleotides which identify and encode EXCS. EXCS can be expressed by standard recombinant methodology. The amino acid and nucleic acid sequences of EXCS are useful for diagnosing, treating and preventing infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke), reproductive (infertility, ovulatory defects, endometriosis), autoimmune/inflammatory (actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease), and cell proliferative disorders including cancers (of the breast, adrenal gland, bone). They may also be used to treat fatal familial insomnia, nutritional and metabolic diseases of the nervous system, myopathies, mental disorders (anxiety, schizophrenia, mood), as well as infections caused by parasites (malaria, leishmania, trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus, blastomycoses, dermatophytes) agents. The nucleic acids, polypeptides, antagonists, agonists, pharmaceutical compositions, and antibodies may also be used for treating or preventing disorders associated with increased or decreased expression or activity of EXCS. EXCS polynucleotides may also be used to detect and quantify gene expression in biopsied tissues in which expression of EXCS may be correlated with the disease, to determine presence or excess expression of EXCS, to monitor regulation of EXCS levels during therapeutic intervention, to detect the presence of associated disorders, as targets in microarray, to generate hybridization probes, and to detect differences in gene sequences among normal carrier or affected individuals. Antibodies may also be used in diagnosing disorders, in monitoring patients being treated with EXCS agonists, antagonists or inhibitors. Sequences AA48057 CC -B48082 represent the EXCS of the invention. | PP 29-JUN-2001; 2001WO-US021066. | XX |
| XX | CC Sequence 179 AA; | XX | XX |
| XX | Query Match 99.3%; Score 897; DB 4; Length 179; | PI Baker KP, Desnoyers L, Gerritsen MB, Godowski PJ; PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI; | XX |
| XX | Best Local Similarity 98.3%; Pred. No. 8-7e-87; | DR WPI: 2002-172001/22. | XX |
| XX | Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0; | DR N-PSDB; ABX33657. | XX |
| XX | 1 MAALQKSVSSFLMGTATLSCILLALLVQGGAAPISSHCRLDKSNFQQPYITINRPFMLA 60 | PT One hundred and twenty two nucleic acids encoding PRO polypeptides, PT useful for treating a PRO related disorder and for diagnosing tumors such PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor PT or liver tumor. | XX |

PS Claim 11; Fig 244; 359pp; English.

CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polymucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including the use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-HAU83713 represent human PRO
 CC protein sequences of the invention

XX Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;

Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTATLATSCLLALLIVQGAAAPISHC3LDKSNFOQPYITNRTFMLA 60
 Db 1 MAALQKSVSSFLMGTATLATSCLLALLIVQGAAAPISHC3LDKSNFOQPYITNRTFMLA 60

Qy 61 KEASLADNNNTDVRLIGKLFHSTMSRCYLMKQVNLTFEVLFLPQSDRFQPYMQEVVP 120
 Db 61 KEASLADNNNTDVRLIGKLFHSTMSRCYLMKQVNLTFEVLFLPQSDRFQPYMQEVVP 120

Qy 121 FLARI5NRLSTCHIEGDDLH1QRNVQKLKDTYKIGSEGEIKAGEDLFLMSLRNACI 179
 Db 121 FLARI5NRLSTCHIEGDDLH1QRNVQKLKDTYKIGSEGEIKAGEDLFLMSLRNACI 179

* Db 121 FLARI5NRLSTCHIEGDDLH1QRNVQKLKDTYKIGSEGEIKAGEDLFLMSLRNACI 179

* Db 121 FLARI5NRLSTCHIEGDDLH1QRNVQKLKDTYKIGSEGEIKAGEDLFLMSLRNACI 179

RESULT 9

BAE19237 standard; protein; 179 AA.

XX

AAE19237;

AC 21-MAY-2002 (first entry)

DE Human TIF protein.

XX Human TIF protein.

XX Human TIF protein.

XX T cell derived inducible factor; TIF; interleukin-21; IL-21; human;
 XX STAT transcription factor; acute phase protein; inflammation;
 XX Chromosome 12.

OS Homo sapiens.

XX WO200210393-A2.

XX 07-FEB-2002.

PD 27-JUN-2001; 2001WO-US020485.

XX 27-JUL-2000; 2000US-00626617.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX Dumoutier L, Renaud J;

XX W21; 2002-195964/25.

DR N-PSDBB; AAD30645.

XX Stimulating expression of STAT transcription factor and inducing
 XX production of acute phase protein in a cell, involves contacting a cell
 XX capable of expressing STAT with T cell derived inducible factors.

PS Disclosure; Page 64; 64pp; English.

XX The invention relates to nucleic acid molecules encoding T cell derived
 CC inducible factors (TIFs) also known as interleukin-21 (IL-21). TIF
 CC polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or IL-21
 CC molecules are implicated in activation of STAT transcription factors.
 CC acute phase proteins and inflammation. The present sequence is human TIF
 CC protein. The TIF gene is located on chromosome 12.

XX SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;

Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTATLATSCLLALLIVQGAAAPISHC3LDKSNFOQPYITNRTFMLA 60

Db 1 MAALQKSVSSFLMGTATLATSCLLALLIVQGAAAPISHC3LDKSNFOQPYITNRTFMLA 60

Qy 61 KEASLADNNNTDVRLIGKLFHSTMSRCYLMKQVNLTFEVLFLPQSDRFQPYMQEVVP 120

Db 61 KEASLADNNNTDVRLIGKLFHSTMSRCYLMKQVNLTFEVLFLPQSDRFQPYMQEVVP 120

RESULT 10

ABG95927 standard; protein; 179 AA.

XX ID ABG95927

AC ABG95927;

XX DT 10-DEC-2002 (first entry)

XX DE Human secreted/transmembrane protein PRO10096.

XX KW Human; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;

KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

OS Homo sapiens.

XX PN US2002119120-A1.

XX PD 29-AUG-2002.

XX PP 06-DEC-2001; 2001US-00006867.

PR 29-OCT-1997; 97US-0063415P.

PR 29-OCT-1997; 97US-0064215P.

PR 22-APR-1998; 98US-0082737P.

PR 29-APR-1998; 98US-0083495P.

PR 15-MAY-1998; 98US-0085579P.

PR 02-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088029P.

PR 11-JUN-1998; 98US-0088030P.

PR 12-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088740P.

PR 17-JUN-1998; 98US-0088811P.

PR 19-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

PR 11-JUN-1998; 98US-0088833P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089633P.

PR 19-JUN-1998; 98US-0089932P.

PR 22-JUN-1998; 98US-0090246P.

PR 24-JUN-1998; 98US-0090444P.

PR 25-JUN-1998; 98US-0090588P.

PR 25-JUN-1998; 98US-0090696P.

Novel isolated interleukin 22 polypeptide useful for identifying IL-22 agonists and antagonists that are used for treating acute pancreatitis, chronic pancreatitis, pancreatic carcinoma, pancreatic carcinoma.

Claim 11; Fig 2; 94pp; English.

The present invention relates to a new polypeptide having at least 80% identity to a 101 amino acid interleukin (IL)-22 sequence. The invention is useful for detecting IL-22 (IL-22 receptor) or IL-10beta polypeptide in a sample which involves contacting sample with an IL-22 polypeptide and determining the formation of an IL-22R/IL-22 polypeptide conjugate or an IL-10beta/IL-22 polypeptide conjugate. Preferably, the IL-22 polypeptide is labelled with a detectable label or is attached to a solid support. The polypeptide is also useful for linking a biactive molecule, to e.g. toxin, radiolabel or antibody that causes the death of the cell, to a cell expressing IL-22R polypeptide or IL-10beta polypeptide which involves contracting the cell with IL-22 polypeptide which is bound to the biactive molecule and allowing binding of the IL-22 polypeptide with IL-22R or IL-10beta polypeptide thus linking the biactive molecules to the cell. The molecules of the invention can also be used for modulating biological activity of cell expressing IL-22R or IL-10beta polypeptide whereby the cell is killed and the antibody of the invention is useful for inhibiting IL-22 induced expression of PAP (pancreatitis associated protein) by pancreatic cells. The antibody is also useful for treating a pancreatic disorder such as acute or chronic pancreatitis, pancreatic carcinoma including acinar cell carcinoma or mixed cell population pancreatic carcinoma and for reducing the activated or inflamed condition of the pancreas in a mammal. The present amino acid sequence represents the human interleukin 22 (IL-22) protein of the invention.

Sequence 179 AA:

| | | | |
|-----------------------|-------|-------------------------------|-------------------|
| Query Match | 99.3% | Score 89%; Pred. No. 8.7e-87; | DB 5; Length 179; |
| Best Local Similarity | 98.3% | | |
| Matches | 176; | Conservative | Indels |

1 MAALQKSSSPMGLATSCILLALLVGGAAPISSHCRLLDKSNFQOP
1 MAALQKSSSPMGLATSCILLALLVGGAAPISSHCRLLDKSNFQOP
1 MAALQKSSSPMGLATSCILLALLVGGAAPISSHCRLLDKSNFQOP

61 XEASLADNTDVRLLIGEKLFGVMSRCYLKQVNLNFTEVLFQSDR
61 XEASLADNTDVRLLIGEKLFGVMSRCYLKQVNLNFTEVLFQSDR
61 XEASLADNTDVRLLIGEKLFGVMSRCYLKQVNLNFTEVLFQSDR

121 **FLARISNRSLSTCHIEGDDDLHQNRVQKLKDUTVKKIGESEGSZIKAGLDLIL**
 121 **FLARISNRSLSTCHIEGDDDLHQNRVQKLKDUTVKKIGESEGSZIKAGLDLIL**

RESULT 1.3
AAE28608

AAA28608 ;
XX
XX
XX
XX

Human IL-TIF protein #1.

inflammatory bowel disease; rheumatoid disease; systemic lupus erythematosus; myasthenia gravis; pan-
diabetes; atherosclerosis; glomerulonephritis; gene therapy

KNN
XX
Homo sapiens.

WO200270655-A2.
12-SEP-2002.

XX 02-MAR-2001; 2001US-0273035P.
 PR 27-MAR-2001; 2001US-0279232P.
 XX
 XX (ZIMC) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
 XX
 DR WPI: 2002-698750/75.
 DR N-PSDB; AAD45964.
 XX
 PT New Zcytor16 polypeptide useful for treating autoimmune or inflammatory
 diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,
 atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects
 of IL-TIF.
 XX
 PT Disclosure; Page 197-198; 221pp; English.
 PS XX
 CC The invention relates to cytokine receptor designated as mouse Zcytor16
 CC which can bind and antagonize the IL-TIF. The Zcytor16 polypeptide is
 CC useful in modulating the immune system by binding Zcytor16 ligand, and
 CC thus, preventing the binding of the ligand with endogenous Zcytor16
 CC receptor. It is useful for studying human inflammation or immune
 CC function, or for treating autoimmune or inflammatory diseases such as
 CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus
 CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,
 CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic
 CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-
 CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the
 CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene
 CC expression and gene structure, such as in the diagnosis and/or prevention
 CC of spontaneous abortions or in monitoring placental health and function.
 CC It is also used in gene therapy. The Present sequence is human IL-TIF
 CC protein.

| XX | Sequence 179 AA; | Score 897; DB 5; Length 179; | QY | Query Match | Best Local Similarity | Score 897; Pred. No. 8 | 7e-87; | XX |
|-----------|------------------|-------------------------------------|-----|--|---------------------------|------------------------|---------------|-------------------|
| SS | | | | | Matches 176; Conservative | 3; | Mismatches 0; | Indels 0; Gaps 0; |
| Db | | | 1 | MAALQKVSSEFLGMLTATSCLLLALLVQGGAAPISCHRLDKSNFQDQYITNRTFMLA | 60 | | | |
| QY | | | 1 | MAALQKVSSEFLGMLTATSCLLLALLVQGGAAPISCHRLDKSNFQDQYITNRTFMLA | 60 | | | |
| Db | | | 61 | KVASLADNNNTDVLIGERLFLRGTYSMSRCYLMQVNLITLEEVLPQSERFQPYMQEVVP | 120 | | | |
| QY | | | 61 | KVASLADNNNTDVLIGERLFLRGTYSMSRCYLMQVNLITLEEVLPQSERFQPYMQEVVP | 120 | | | |
| Db | | | 121 | FIARISNRLLSTCHIGDDLHICRNVQKLKDTRVKGESBEIAKGEDLILFMSLRNACI | 179 | | | |
| QY | | | 121 | FIARISNRLLSTCHIGDDLHICRNVQKLKDTRVKGESBEIAKGEDLILFMSLRNACI | 179 | | | |
| Db | | | 121 | PLARLSNRLLSTCHIGDDLHICRNVQKLKDTRVKGESBEIAKGEDLILFMSLRNACI | 179 | | | |
| RESULT 14 | | | | | | | | |
| XX | AAU76909 | AAU76909 standard; protein; 179 AA. | XX | AAU76909; | | | | |
| XX | XX | | AC | AAU76909; | | | | |
| DT | 05-JUN-2002 | {first entry} | XX | | | | | |
| XX | | | DB | Human interleukin-T-cell inducible factor (IL-TIF). | | | | |
| XX | | | XX | Z-Cytokine II; human; cytokine receptor; atopy; psoriasis; | | | | |
| XX | | | XX | interleukin-T-cell inducible factor; IL-TIF; allergy; asthma; | | | | |
| XX | | | XX | receptor-modulated apoptosis; Th1; immune response; pancreatitis; | | | | |
| XX | | | XX | type I diabetes; IDDM; pancreatic cancer; Graves disease; SLB; | | | | |
| XX | | | XX | inflammatory bowel disease; IBD; Crohn's disease; colon cancer; | | | | |
| XX | | | XX | intestinal cancer; diverticulitis; autoimmune disease; sepsis; | | | | |
| XX | | | XX | multiple sclerosis; MS; systemic lupus erythematosus; myasthenia gravis; | | | | |
| XX | | | XX | rheumatoid arthritis; kidney dysfunction. | | | | |

| | | | |
|--------------------------|--|-------------------------------|---|
| OS | Homo sapiens. | XX | ABB95599 standard; protein; 179 AA. |
| BN | WC200212345-A2. | AC | ABB95599; |
| XX | | AC | |
| XX | 14-FEB-2002. | XX | 19-JUL-2002 (first entry) |
| PF | 08-AUG-2001; 2001WO-US024838. | DE | Human angiogenesis related protein PRO10096 SEQ ID NO: 354. |
| XX | | XX | |
| PR | 08-AUG-2000; 2000US-0223827P. | XX | Human; angiogenesis; PRO protein; cardiovascular; wound; cancer; |
| PR | 01-DEC-2000; 2000US-0250876P. | KW | atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; |
| XX | | KW | cardiant; cytostatic; antiangiogenic; hypotensive; pulmonary; |
| (ZM0) ZYMOGENETICS INC. | | KW | antiarteriosclerotic. |
| XX | | XX | |
| PL | Kindsvogel WR, Topouzis S; | OS | Homo sapiens. |
| XX | | XX | |
| DR | WPI; 2002-217182/27. | PN | WO200208284-A2. |
| XX | | XX | |
| PR | New soluble cytokine receptor which binds interleukin-T-cell inducible | XX | 31-JAN-2002. |
| PR | factor and antagonizes its activity in inflammatory and immune diseases | XX | PD |
| PR | such as cancer, diabetes, asthma, sepsis, psoriasis and autoimmune | XX | 09-JUL-2001; 2001WO-US021735. |
| PR | diseases. | XX | PR |
| XX | | XX | 20-JUL-2000; 2000US-0219556P. |
| PS | Example 2; Page 98; 117pp; English. | PR | PR |
| XX | | 25-JUL-2000; 2000US-022024P. | PR |
| CC | This invention relates to the protein and cDNA sequences of a novel | PR | 25-JUL-2000; 2000US-0220664P. |
| CC | soluble cytokine receptor polypeptide designated zcytorII, which binds | PR | PR |
| CC | interleukin-T-cell inducible factor (IL-TIF) or antagonises IL-TIF or | 28-JUL-2000; 2000WO-US020210. | PR |
| CC | IL-9 induced inflammation, and inhibiting IL-TIF induced proliferation | PR | 02-AUG-2000; 2000US-0222959P. |
| CC | activity. The protein of the invention is useful for reducing IL-TIF- or | PR | 17-AUG-2000; 2000US-001643657. |
| CC | IL-9 induced inflammation, and inhibiting IL-TIF induced proliferation | PR | 23-OCT-2000; 2000WO-US023522. |
| CC | or the protein is also useful for suppressing an immune response in a mammal | PR | 24-AUG-2000; 2000WO-US023328. |
| CC | exposed to an antigen or pathogen. Soluble zcytorII receptor or | PR | 07-SEP-2000; 2000US-0230978P. |
| CC | heterodimeric polypeptide is useful for enhancing the in-vivo killing of | PR | 18-SEP-2000; 2000US-001664610. |
| CC | target tissues by directly stimulating a zcytorII receptor-modulated | PR | 18-SEP-2000; 2000US-001663350. |
| CC | apoptotic pathway. IL-TIF is involved in promoting Th1-type immune | PR | 24-OCT-2000; 2000US-0242922P. |
| CC | responses and antagonists of IL-TIF have beneficial effect against diseases | PR | 38-NOV-2000; 2000WO-US0709238. |
| CC | involving such immune responses. Soluble zcytorII heterodimers are useful | PR | 08-NOV-2000; 2000WO-US030952. |
| CC | as antagonists in inflammatory and immune diseases or conditions such as | PR | 10-NOV-2000; 2000WO-US0309873. |
| CC | pancreatitis, type I diabetes (IDDM), pancreatic cancer, Graves disease, | PR | 01-DEC-2000; 2000WO-US034678. |
| CC | inflammatory bowel disease (IBD), Crohn's disease, colon and intestinal | PR | 20-DEC-2000; 2000US-001747259. |
| CC | cancer, diverticulosis, autoimmune disease (e.g. IDDM, multiple sclerosis | PR | 22-JAN-2001; 2000US-001767609. |
| CC | (MS), systemic lupus erythematosus (SLE), myasthenia gravis, rheumatoid | PR | 28-FEB-2001; 2001US-00798498. |
| CC | arthritis and IBD), sepsis, asthma and other atopic diseases, | PR | 28-FEB-2001; 2001WO-US-0004520. |
| CC | psoriasis and kidney dysfunction. Soluble zcytorII receptor or | PR | 01-MAR-2001; 2001WO-US006666. |
| CC | heterodimeric receptor polypeptides are useful in vivo or in diagnostic | PR | 09-MAR-2001; 2001US-00802206. |
| CC | applications to detect IL-TIF expressing cancers in vivo or in tissue | PR | 22-MAR-2001; 2001US-00804689. |
| CC | samples and to prepare antibodies. ZcytorII serves as a target for Mab | PR | 05-APR-2001; 2001US-00816744. |
| CC | therapy of cancer where an antagonising Mab inhibits cancer growth and | PR | 10-MAY-2001; 2001US-00854408. |
| CC | targets immune-mediated killing. The present sequence represents the | PR | 10-MAY-2001; 2001US-00854280. |
| CC | interleukin-T-cell inducible factor (IL-TIF) protein, the activity of | PR | 25-MAY-2001; 2001US-00866028. |
| XX | this protein is inhibited by the zcytorII protein of the invention | PR | 25-MAY-2001; 2001WO-US017800. |
| SD | Sequence 179 AA; | PR | 30-MAY-2001; 2001US-00870574. |
| SD | Query Match 99.3%; Score 397; DB 5; Length 179; | PR | 30-MAY-2001; 2001WO-US017443. |
| SD | Best Local Similarity 98.3%; Pred. No. 8.7e-87; | PR | 01-JUN-2001; 2001WO-US017800. |
| SD | Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0; | PR | 20-JUN-2001; 2001WO-US019692. |
| Qy | 1 MAALQKSYSSFLGTLATSCLLLALIVGGAAAPISHSICRDKSNEFCQPYITNRTFVLA 60 | XX | XX (GETH) GENENTECH INC. |
| Db | 1 MAALQKSYSSFLGTLATSCLLLALIVGGAAAPISHSICRDKSNEFCQPYITNRTFVLA 60 | PA | PA (BAKE/) BAKER K P. |
| Qy | 61 KEASLADNNTDVRLIGEKFHGVSMSRCYLMKVNFLEEVLFQSDRFQPMQEVYV 120 | PA | PA (FERR/) FERRARA N. |
| Db | 61 KEASLADNNTDVRLIGEKFHGVSMSRCYLMKVNFLEEVLFQSDRFQPMQEVYV 120 | PA | PA (GERB/) GERBER H. |
| Qy | 121 FIASRNLSTCHLEGDLHIIQRNVQKLKDTVKXIGESEBIAIGELDLLFMSLRNACI 179 | PA | PA (GERR/) GERRITSEN M E. |
| Db | 121 FLARLSNLSTCHLEGDLHIIQRNVQKLKDTVKXIGESEBIAIGELDLLFMSLRNACI 179 | PA | PA (GODD/) GODDARD A. |
| Qy | 121 FLARLSNLSTCHLEGDLHIIQRNVQKLKDTVKXIGESEBIAIGELDLLFMSLRNACI 179 | PA | PA (GODO/) GODOWSKI P J. |
| Db | 121 FLARLSNLSTCHLEGDLHIIQRNVQKLKDTVKXIGESEBIAIGELDLLFMSLRNACI 179 | PA | PA (GURN/) GURNEY A L. |
| PA | PA (HILL/) HILLIAN K J. | PA | PA (HILL/) HILLIAN K J. |
| PA | PA (MARS/) MARSTERS S A. | PA | PA (MARS/) MARSTERS S A. |
| PA | PA (PANI/) PAN J. | PA | PA (PANI/) PAN J. |
| PA | PA (PAON/) PAONI N F. | PA | PA (PAON/) PAONI N F. |
| PA | PA (STEP/) STEPHAN J F. | PA | PA (STEP/) STEPHAN J F. |
| PA | PA (WATA/) WATANABE C K. | PA | PA (WATA/) WATANABE C K. |
| PA | PA (WILL/) WILLIAMS P M. | PA | PA (WILL/) WILLIAMS P M. |
| PA | PA (WON/) WCON W T. | PA | PA (WON/) WCON W T. |

RESULT 15
A8B95599

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PT Stephan JP, Watanabe CK, Williams PW, Wood WI, Ye W;
 XX DR WPI; 2002-171999/22;
 DR N-PSDB; ABL95737/

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

PS Claim 11; FIG 354; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related muscular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention

XX SQ Sequence 179 AA;

| | | | | |
|-----------------------|--|--------------------|---------------|-------------|
| Query Match | 99.3% | Score 897; | DB 5; | Length 179; |
| Best Local Similarity | 98.3% | Pred. No. 8.7e-87; | | |
| Matches 176; | Conservative | 3; | Mismatches 0; | Indels 0; |
| Db | | | Gaps 0; | |
| Qy | 1 MAALQKSSSPFLNGTLADSCLLALLVQGGAAPISHCRLDKSNPQPYTTNRTMIA 60 | | | |
| Db | 1 MAALQKSSSPFLNGTLADSCLLALLVQGGAAPISHCRLDKSNPQPYTTNRTMIA 60 | | | |
| Qy | 61 KERASLADNTDVLIGELFHGVSMSECYLMEKQVLTLEEVLFQSDRFOPYMQEYVP 120 | | | |
| Db | 61 KERASLADNTDVLIGELFHGVSMSECYLMEKQVLTLEEVLFQSDRFOPYMQEYVP 120 | | | |
| Qy | 121 FLARISNLSTCHIEGDPLHIONVQKLKDTVKIGIGEIKAGEIQLLPMSLRNACI 179 | | | |
| Db | 121 FLARISNLSTCHIEGDPLHIONVQKLKDTVKIGIGEIKAGEIQLLPMSLRNACI 179 | | | |

Search completed: June 30, 2004, 19:28:45
 Job time : 62 secs